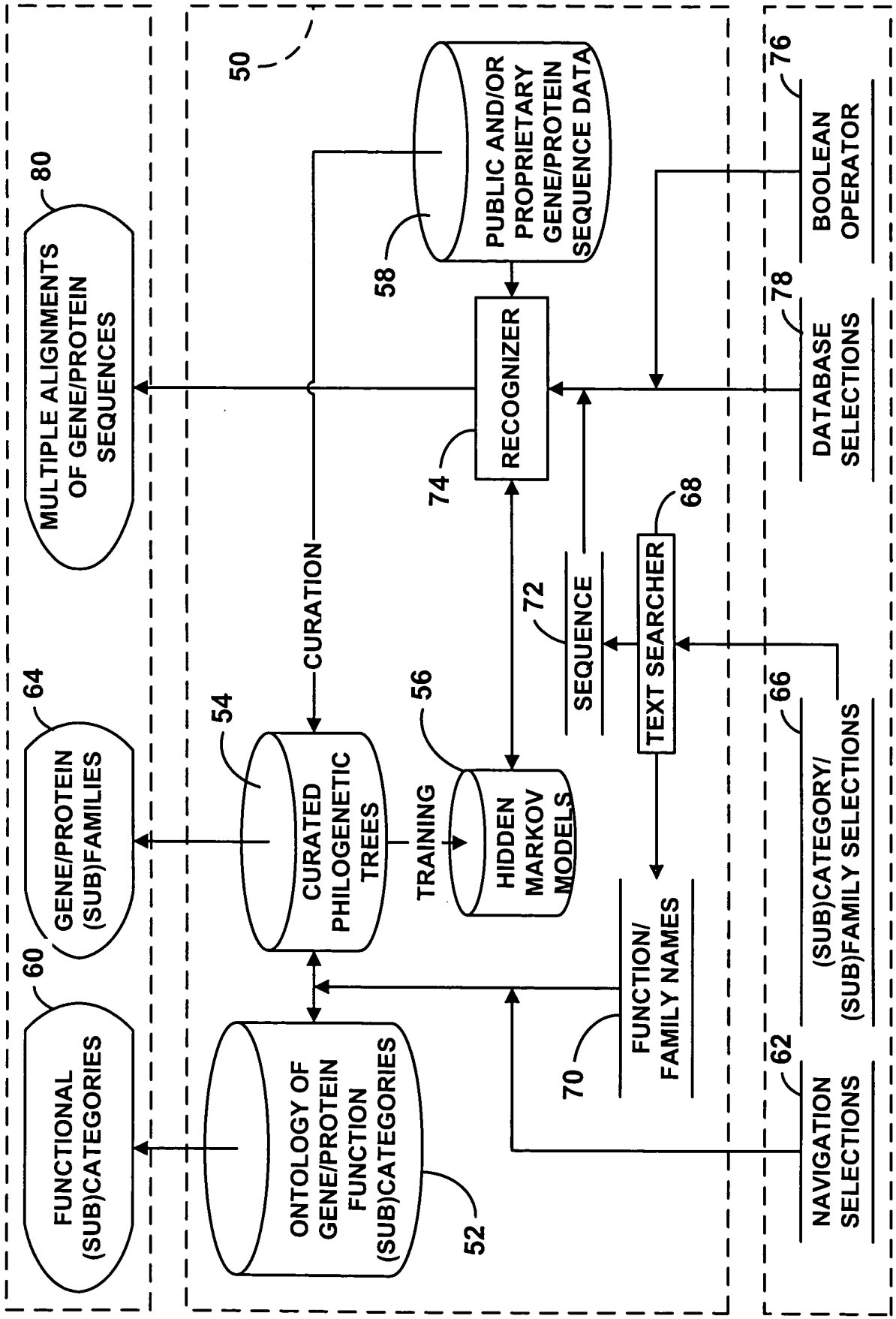

50
80
MULTIPLE ALIGNMENTS OF GENE/PROTEIN SEQUENCES
58
PUBLIC AND/OR PROPRIETARY GENE/PROTEIN SEQUENCE DATA
76
BOOLEAN OPERATOR
78
DATABASE SELECTIONS
74
RECOGNIZER
CURATION
64
GENE/PROTEIN (SUB)FAMILIES
54
CURATED PHILOGENETIC TREES
56
TRAINING
HIDDEN MARKOV MODELS
72
SEQUENCE
68
TEXT SEARCHER
66
(SUB)CATEGORY/ (SUB)FAMILY SELECTIONS
60
FUNCTIONAL (SUB)CATEGORIES
ONTOLOGY OF GENE/PROTEIN FUNCTION (SUB)CATEGORIES
52
70
FUNCTION/ FAMILY NAMES
62
NAVIGATION SELECTIONS

Figure - 1

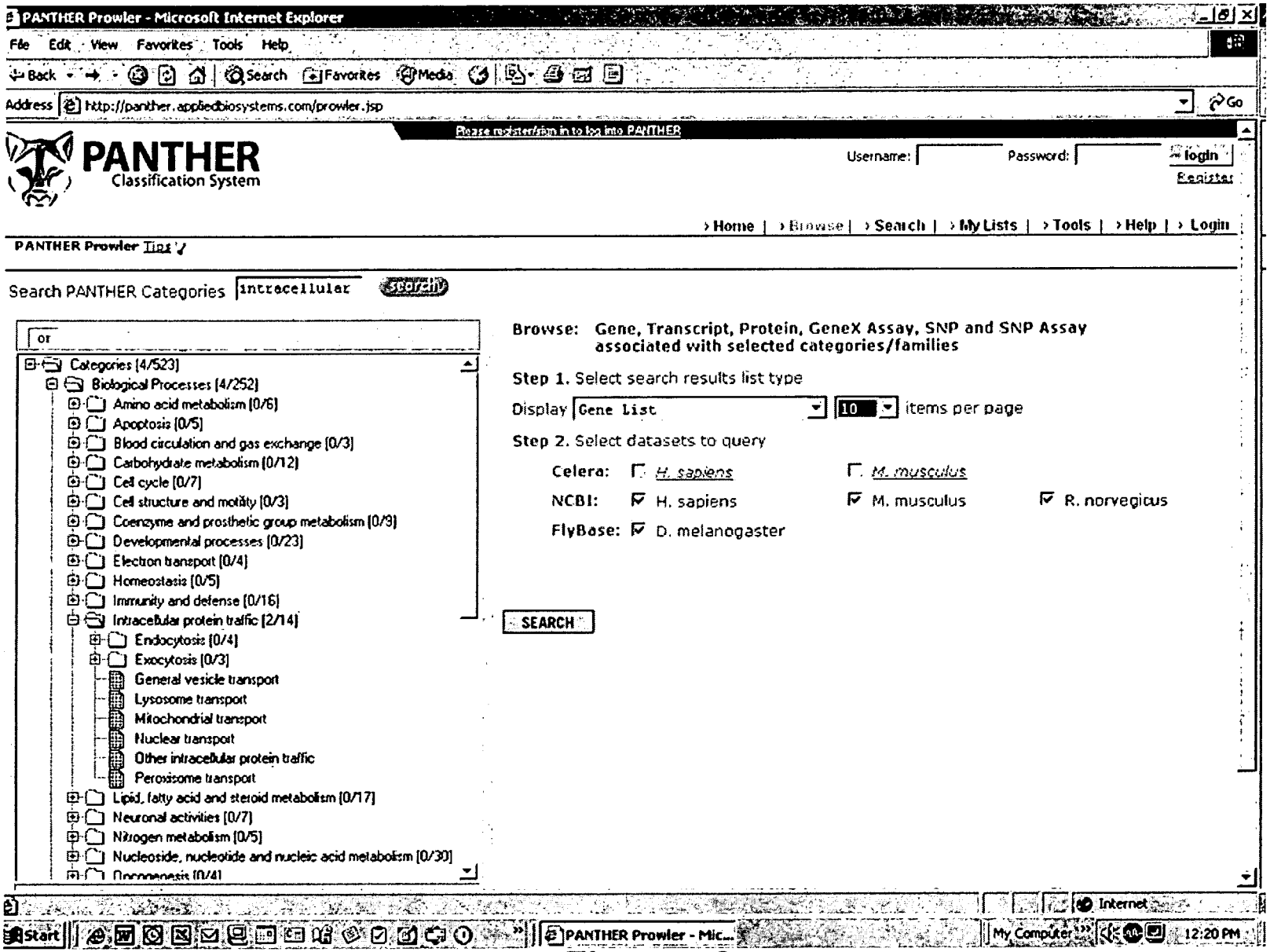

PANTHER Prowler - Microsoft Internet Explorer
File Edit View Favorites Tools Help
Address http://panther.appliedbiosystems.com/prowler.jsp
PANTHER Classification System
Username: Password: login
Register
› Home | › Browse | › Search | › My Lists | › Tools | › Help | › Login
PANTHER Prowler Tips
Search PANTHER Categories intracellular Search
Browse: Gene, Transcript, Protein, GeneX Assay, SNP and SNP Assay associated with selected categories/families
Step 1. Select search results list type
Display Gene List 10 items per page
Step 2. Select datasets to query
Celera: H. sapiens M. musculus
NCBI: H. sapiens M. musculus R. norvegicus
FlyBase: D. melanogaster
SEARCH
Categories [4/523]
Biological Processes [4/252]
Amino acid metabolism [0/6]
Apoptosis [0/5]
Blood circulation and gas exchange [0/3]
Carbohydrate metabolism [0/12]
Cell cycle [0/7]
Cell structure and motility [0/3]
Coenzyme and prosthetic group metabolism [0/9]
Developmental processes [0/23]
Electron transport [0/4]
Homeostasis [0/5]
Immunity and defense [0/16]
Intracellular protein traffic [2/14]
Endocytosis [0/4]
Exocytosis [0/3]
General vesicle transport
Lysosome transport
Mitochondrial transport
Nuclear transport
Other intracellular protein traffic
Peroxisome transport
Lipid, fatty acid and steroid metabolism [0/17]
Neuronal activities [0/7]
Nitrogen metabolism [0/5]
Nucleoside, nucleotide and nucleic acid metabolism [0/30]
Start
PANTHER Prowler - Mic...
My Computer
12:20 PM

Figure - 2

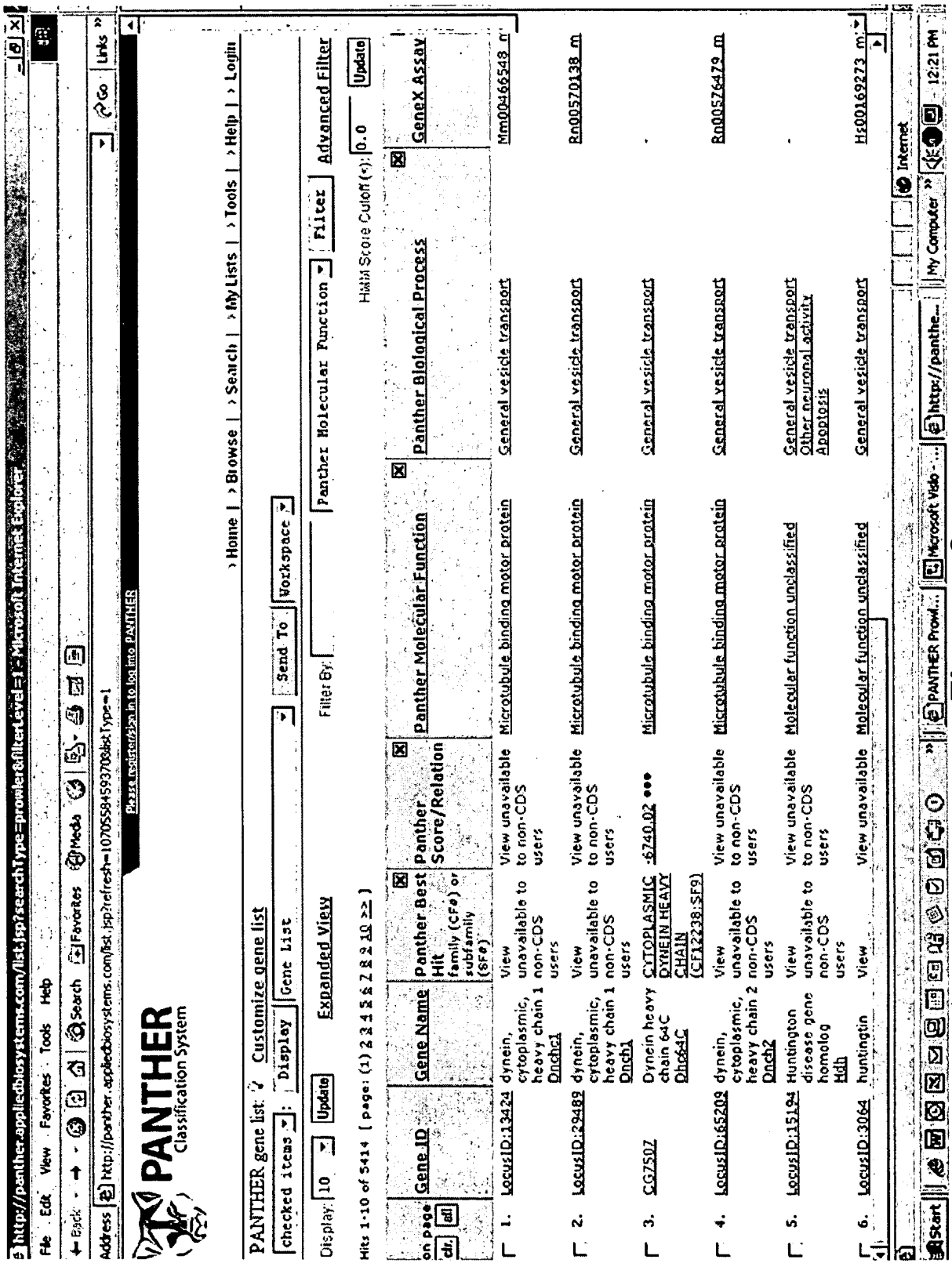

PANTHER
Classification System
› Home | › Browse | › Search | › MyLists | › Tools | › Help | › Login
PANTHER gene list: Customize gene list
Display
Gene List
Send To
Workspace
Filter By:
Panther Molecular Function
Filter
Advanced Filter
Display: 10
Update
Expanded View
Hmm Score Cutoff (≤): 0.0
Update
Hits 1-10 of 5414 [page: (1) 2 3 4 5 6 7 8 9 10 >>]
Gene ID
Gene Name
Panther Best Hit family (CFe) or subfamily (SFe)
Panther Score/Relation
Panther Molecular Function
Panther Biological Process
GeneX Assay
1. LocusID:13424 dynein, cytoplasmic, heavy chain 1 Dnchc1 View unavailable to non-CDS users Microtubule binding motor protein General vesicle transport Mm00466548_m
2. LocusID:29489 dynein, cytoplasmic, heavy chain 1 Dnchc1 View unavailable to non-CDS users Microtubule binding motor protein General vesicle transport Rn00570138_m
3. CG7507 Dynein heavy chain 64C Dhc64C CYTOPLASMIC DYNEIN HEAVY CHAIN (CF12238:SF9) -6740.02 ●●● Microtubule binding motor protein General vesicle transport -
4. LocusID:65209 dynein, cytoplasmic, heavy chain 2 Dnchc2 View unavailable to non-CDS users Microtubule binding motor protein General vesicle transport Rn00576472_m
5. LocusID:15194 Huntington disease gene homolog Hdh View unavailable to non-CDS users Molecular function unclassified General vesicle transport
Other neuronal activity
Apoptosis -
6. LocusID:3064 huntingtin View unavailable Molecular function unclassified General vesicle transport Hs00169273_m1

Figure - 3

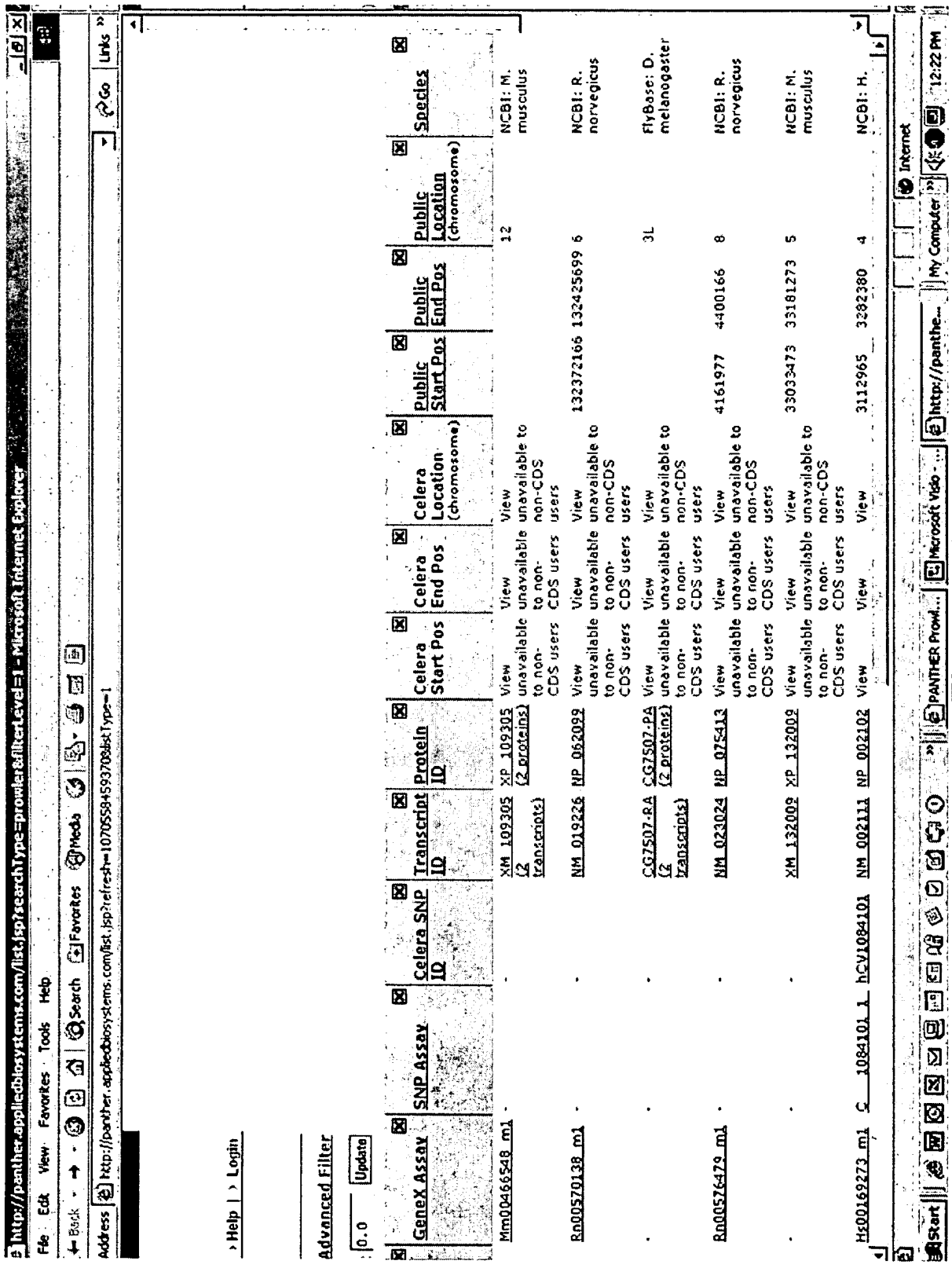

http://panther.appliedbiosystems.com/list.jsp?searchType=prowler&filterLevel=1 - Microsoft Internet Explorer
File Edit View Favorites Tools Help
Address http://panther.appliedbiosystems.com/list.jsp?refresh=1070558459370&listType=1
Links
Help | Login
Advanced Filter
0.0
Update
GeneX Assay
SNP Assay
Celera SNP ID
Transcript ID
Protein ID
Celera Start Pos
Celera End Pos
Celera Location (chromosome)
Public Start Pos
Public End Pos
Public Location (chromosome)
Species
Mm00466548_m1 - XM_109305 (2 transcripts) XP_109305 (2 proteins) View unavailable to non-CDS users View unavailable to non-CDS users View unavailable to non-CDS users 12 NCBI: M. musculus
Rn00570138_m1 - NM_019226 NP_062099 View unavailable to non-CDS users View unavailable to non-CDS users View unavailable to non-CDS users 132372166 132425699 6 NCBI: R. norvegicus
- - CG7507-RA (2 transcripts) CG7507-PA (2 proteins) View unavailable to non-CDS users View unavailable to non-CDS users View unavailable to non-CDS users 3L FlyBase: D. melanogaster
Rn00576479_m1 - NM_023024 NP_075413 View unavailable to non-CDS users View unavailable to non-CDS users View unavailable to non-CDS users 4161977 4400166 8 NCBI: R. norvegicus
- - XM_132009 XP_132009 View unavailable to non-CDS users View unavailable to non-CDS users View unavailable to non-CDS users 33033473 33181273 5 NCBI: M. musculus
Hs00169273_m1 C__1084101_1 hCV1084101 NM_002111 NP_002102 View View View 3112965 3282380 4 NCBI: H.
Start
PANTHER Prowl...
Microsoft Vido ...
http://panthe...
My Computer
Internet
12:22 PM

Figure - 4

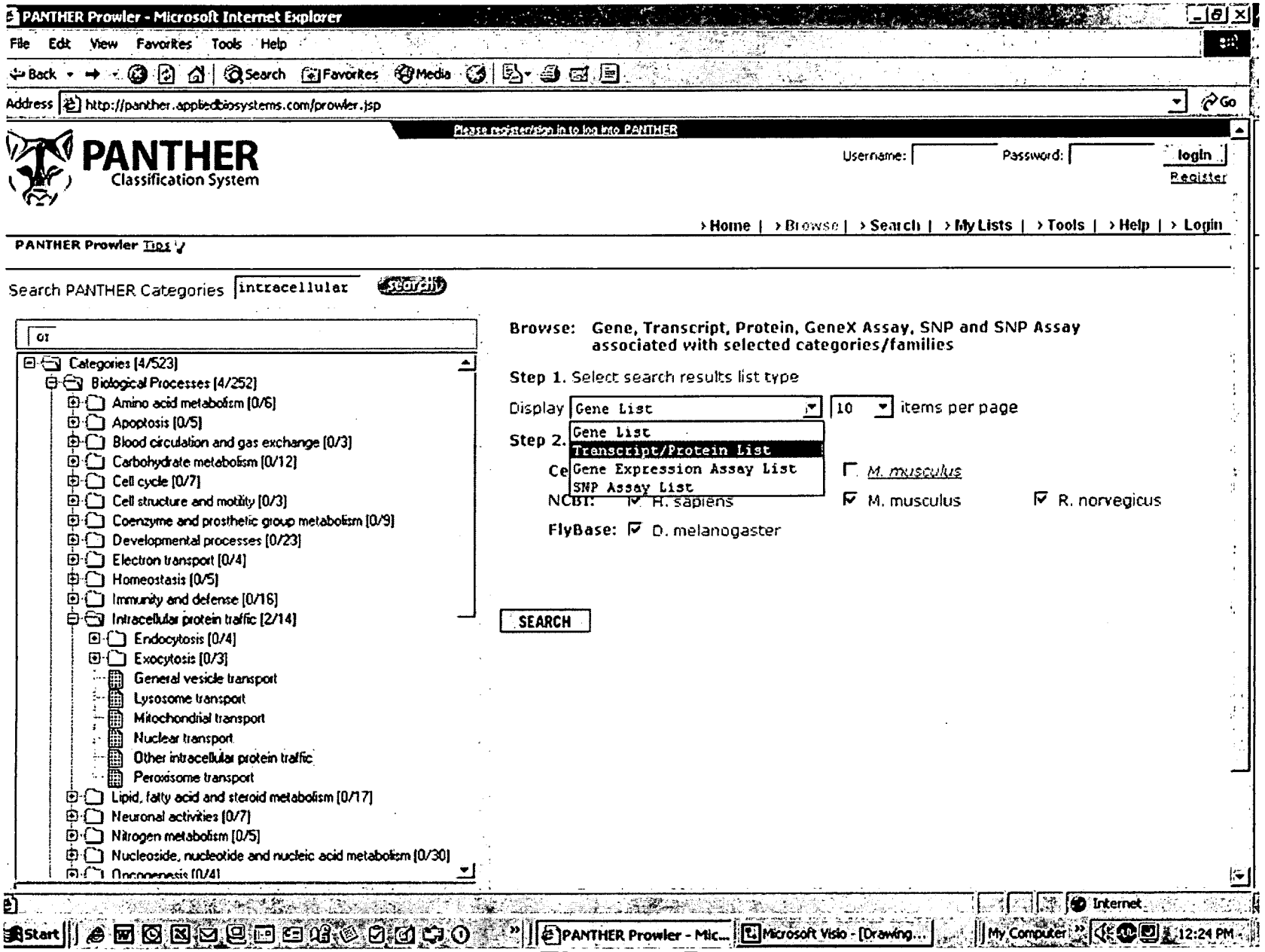

PANTHER Prowler - Microsoft Internet Explorer
File Edit View Favorites Tools Help
Back Search Favorites Media
Address http://panther.appliedbiosystems.com/prowler.jsp
Please register/sign in to log into PANTHER
PANTHER Classification System
Username: Password: login
Register
› Home | › Browse | › Search | › My Lists | › Tools | › Help | › Login
PANTHER Prowler Tips
Search PANTHER Categories intracellular search
Categories [4/523]
Biological Processes [4/252]
Amino acid metabolism [0/6]
Apoptosis [0/5]
Blood circulation and gas exchange [0/3]
Carbohydrate metabolism [0/12]
Cell cycle [0/7]
Cell structure and motility [0/3]
Coenzyme and prosthetic group metabolism [0/9]
Developmental processes [0/23]
Electron transport [0/4]
Homeostasis [0/5]
Immunity and defense [0/16]
Intracellular protein traffic [2/14]
Endocytosis [0/4]
Exocytosis [0/3]
General vesicle transport
Lysosome transport
Mitochondrial transport
Nuclear transport
Other intracellular protein traffic
Peroxisome transport
Lipid, fatty acid and steroid metabolism [0/17]
Neuronal activities [0/7]
Nitrogen metabolism [0/5]
Nucleoside, nucleotide and nucleic acid metabolism [0/30]
Oncogenesis [0/4]
Browse: Gene, Transcript, Protein, GeneX Assay, SNP and SNP Assay associated with selected categories/families
Step 1. Select search results list type
Display Gene List 10 items per page
Gene List
Transcript/Protein List
Gene Expression Assay List
SNP Assay List
Step 2.
Ce
M. musculus
NCBI: H. sapiens M. musculus R. norvegicus
FlyBase: D. melanogaster
SEARCH
Internet
Start
PANTHER Prowler - Mic...
Microsoft Visio - [Drawing...
My Computer
12:24 PM

Figure - 5

http://panther.appliedbiosystems.com/list.jsp?searchType=prowler&filterLevel=1 - Microsoft Internet Explorer
File Edit View Favorites Tools Help
Address http://panther.appliedbiosystems.com/list.jsp?refresh=1070558681239&btType=2
PANTHER Classification System
Please register/sign in to log into PANTHER
› Home | › Browse | › Search | › My Lists | › Tools | › Help | › Login
PANTHER transcript list
Customize transcript list
checked items
Display
Transcript/Protein List
Send To
Workspace
Display 10
Update
Expanded View
Filter By
Protein ID
Filter
Advanced Filter
Hits 1-10 of 6271 (page: (1) 2 3 4 5 6 7 8 9 10 >>)
HMM Score Cutoff (>): 0.0
Update
on page dir. all
Transcript ID
Protein ID
Gene ID
Gene Name
Panther Best Hit family (CF#) or subfamily (SF#)
Panther Score/Relation
Panther Molecular Function
Panther Biological Process
GeneX Assa
1. XM_109305 XP_109305 LocusID:13424 dynein, cytoplasmic, heavy chain 1 Dnchc1 View unavailable to non-CDS users Microtubule binding motor protein General vesicle transport -
2. NM_030238 NP_084514 LocusID:13424 dynein, cytoplasmic, heavy chain 1 Dnchc1 View unavailable to non-CDS users Microtubule binding motor protein General vesicle transport Mm00466548
3. NM_018226 NP_062099 LocusID:29489 dynein, cytoplasmic, heavy chain 1 Dnch1 View unavailable to non-CDS users Microtubule binding motor protein General vesicle transport Rn00570138
4. CGZ507-RA CGZ507-PA CGZ507 Dynein heavy chain 64C Dhc64C CYTOPLASMIC DYNEIN HEAVY CHAIN (CF12238:SF9) -6740.02 ••• Microtubule binding motor protein General vesicle transport -
5. NM_023024 NP_075413 LocusID:65209 dynein, cytoplasmic, View unavailable to non-CDS Microtubule binding motor protein General vesicle transport Rn00576479
Start
PANTHER Prowl...
Microsoft Visio - ...
http://panthe...
My Computer
Internet
12:25 PM

Figure - 6

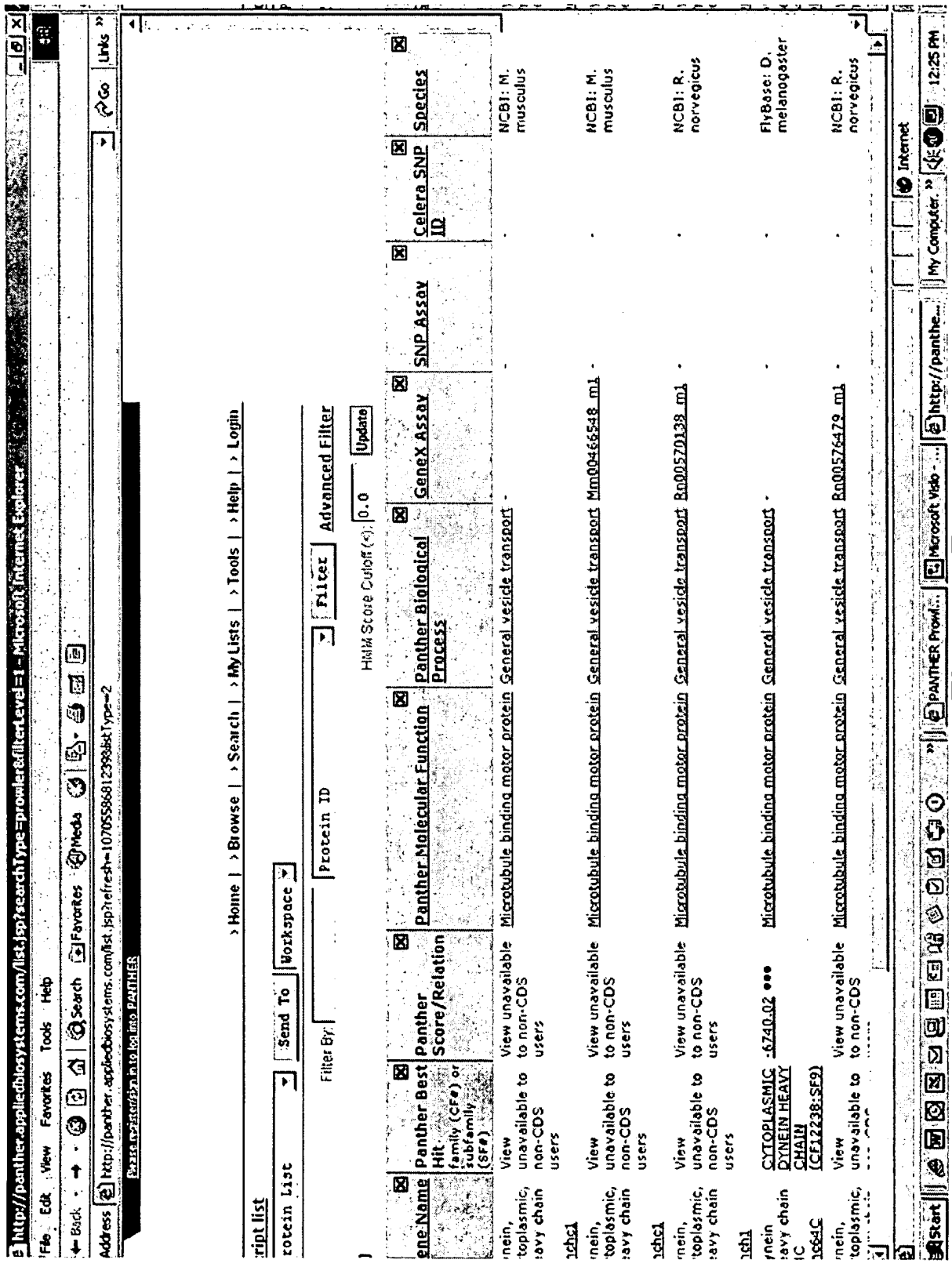

http://panther.appliedbiosystems.com/list.jsp?searchType=prowler&filterLevel=1 - Microsoft Internet Explorer
File Edit View Favorites Tools Help
Address http://panther.appliedbiosystems.com/list.jsp?refresh=1070558681239&listType=2
Links
Please register/sign in to log into PANTHER
› Home | › Browse | › Search | › My Lists | › Tools | › Help | › Login
ript list
rotein List
Send To
Workspace
Filter By:
Protein ID
Filter
Advanced Filter
HMM Score Cutoff (>): 0.0
Update
ene Name
Panther Best Hit family (CF#) or subfamily (SF#)
Panther Score/Relation
Panther Molecular Function
Panther Biological Process
GeneX Assay
SNP Assay
Celera SNP ID
Species
tein, toplasmic, avy chain
View unavailable to non-CDS users
Microtubule binding motor protein
General vesicle transport
NCBI: M. musculus
1dhc1
Mm00466548_m1
1dhc1
Rn00570138_m1
NCBI: R. norvegicus
1dh1
CYTOPLASMIC DYNEIN HEAVY CHAIN (CF12238:SF2)
-6740.02
Rn00576479_m1
FlyBase: D. melanogaster
1664C
Start
PANTHER Prowl...
Microsoft Visio - ...
http://panthe...
My Computer
Internet
12:25 PM

Figure - 7

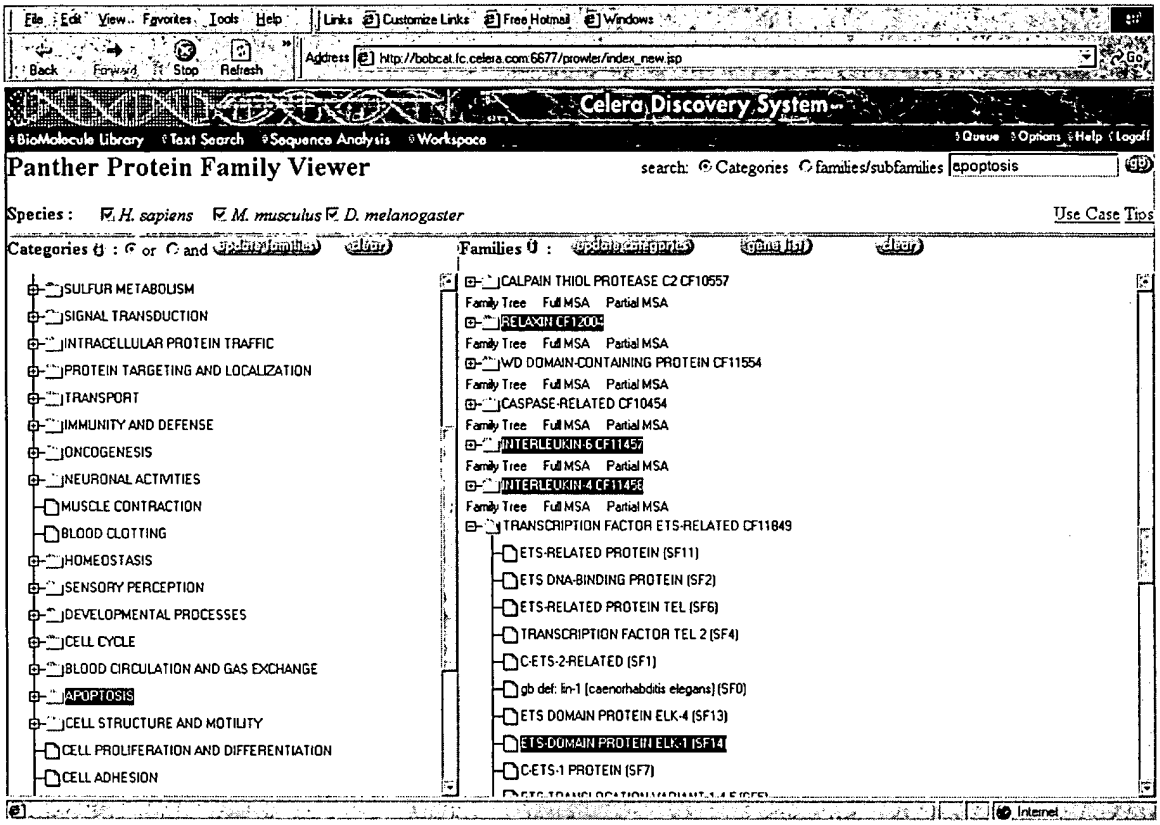


Figure - 8

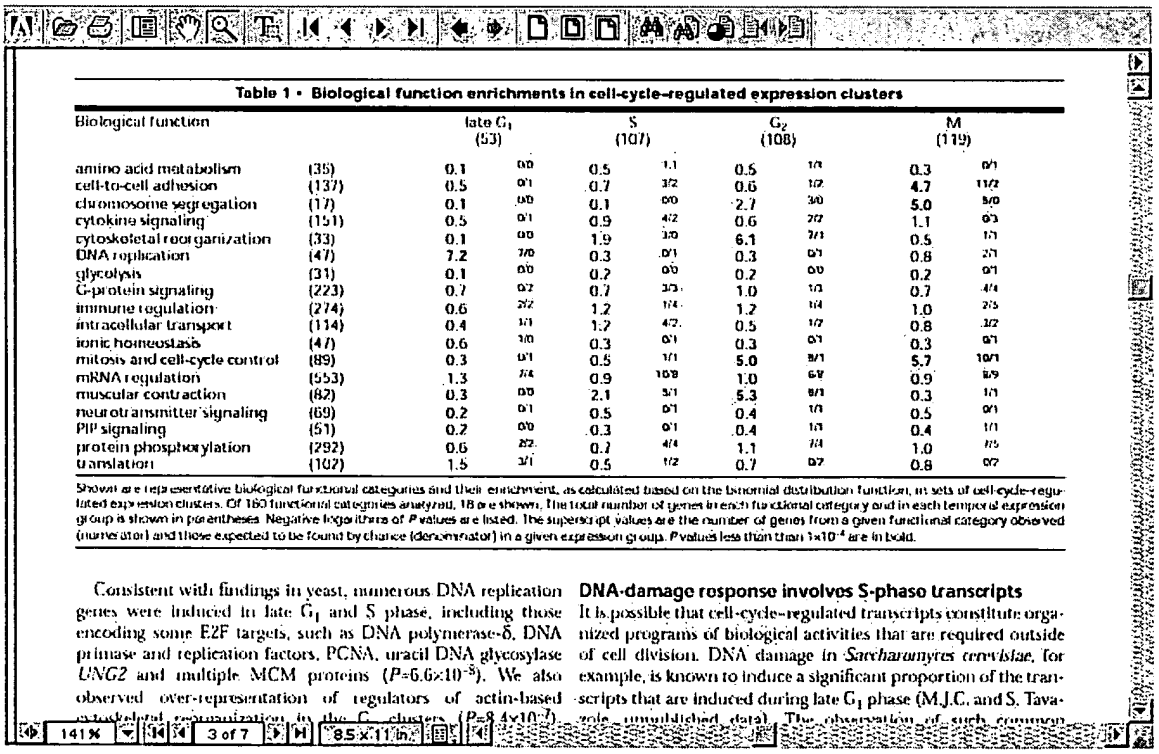


Table 1 • Biological function enrichments in cell-cycle–regulated expression clusters

Biological function		late G_1 (53)		S (107)		G_2 (108)		M (119)	
amino acid metabolism	(35)	0.1	0/0	0.5	1/1	0.5	1/1	0.3	0/1
cell-to-cell adhesion	(137)	0.5	0/1	0.7	1/2	0.6	1/2	4.7	11/2
chromosome segregation	(17)	0.1	0/0	0.1	0/0	2.7	3/0	5.0	5/0
cytokine signaling	(151)	0.5	0/1	0.9	4/2	0.6	2/2	1.1	0/3
cytoskeletal reorganization	(33)	0.1	0/0	1.9	3/0	6.1	3/1	0.5	1/1
DNA replication	(47)	7.2	7/0	0.3	0/1	0.3	0/1	0.8	2/1
glycolysis	(31)	0.1	0/0	0.2	0/0	0.2	0/0	0.2	0/1
G-protein signaling	(223)	0.7	0/2	0.7	3/3	1.0	1/3	0.7	4/4
immune regulation	(274)	0.6	2/2	1.2	7/4	1.2	3/4	1.0	2/5
intracellular transport	(114)	0.4	1/1	1.2	4/2	0.5	1/2	0.8	3/2
ionic homeostasis	(47)	0.6	1/0	0.3	0/1	0.3	0/1	0.3	0/1
mitosis and cell-cycle control	(89)	0.3	0/1	0.5	1/1	5.0	8/1	5.7	10/1
mRNA regulation	(553)	1.3	7/4	0.9	10/8	1.0	6/8	0.9	8/9
muscular contraction	(82)	0.3	0/0	2.1	5/1	5.3	8/1	0.3	1/1
neurotransmitter signaling	(69)	0.2	0/1	0.5	0/1	0.4	1/1	0.5	0/1
PIP signaling	(51)	0.2	0/0	0.3	0/1	0.4	1/1	0.4	1/1
protein phosphorylation	(292)	0.6	2/2	0.7	4/4	1.1	3/4	1.0	3/5
translation	(102)	1.5	3/1	0.5	1/2	0.7	0/2	0.8	0/2

Shown are representative biological functional categories and their enrichment, as calculated based on the binomial distribution function, in sets of cell-cycle–regulated expression clusters. Of 160 functional categories analyzed, 18 are shown. The total number of genes in each functional category and in each temporal expression group is shown in parentheses. Negative logarithms of *P* values are listed. The superscript values are the number of genes from a given functional category observed (numerator) and those expected to be found by chance (denominator) in a given expression group. *P* values less than than 1×10^{-4} are in bold.

Consistent with findings in yeast, numerous DNA replication genes were induced in late G_1 and S phase, including those encoding some E2F targets, such as DNA polymerase-δ, DNA primase and replication factors, PCNA, uracil DNA glycosylase *UNG2* and multiple MCM proteins ($P=6.6\times10^{-5}$). We also observed over-representation of regulators of actin-based cytoskeletal reorganization in the G$_2$ cluster ($P=8.4\times10^{-7}$).

DNA-damage response involves S-phase transcripts

It is possible that cell-cycle–regulated transcripts constitute organized programs of biological activities that are required outside of cell division. DNA damage in *Saccharomyces cerevisiae*, for example, is known to induce a significant proportion of the transcripts that are induced during late G_1 phase (M.J.C. and S. Tavazoie, unpublished data). The observation of such common

Figure - 9

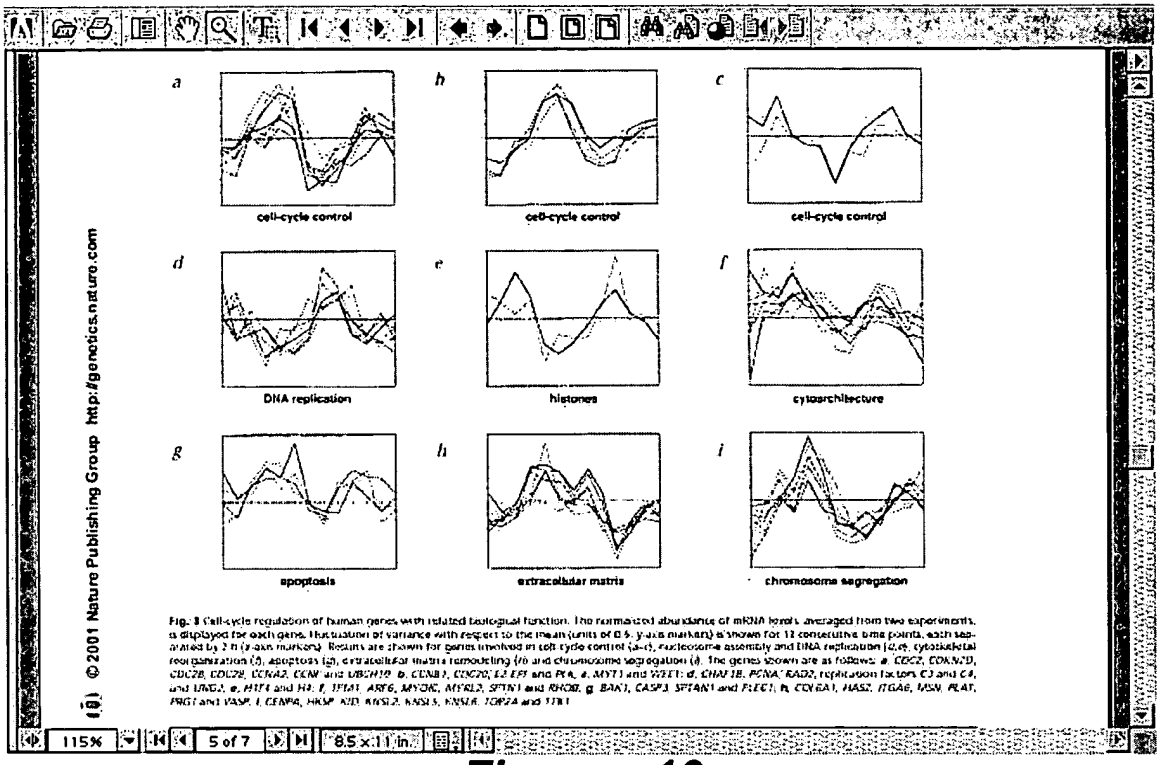
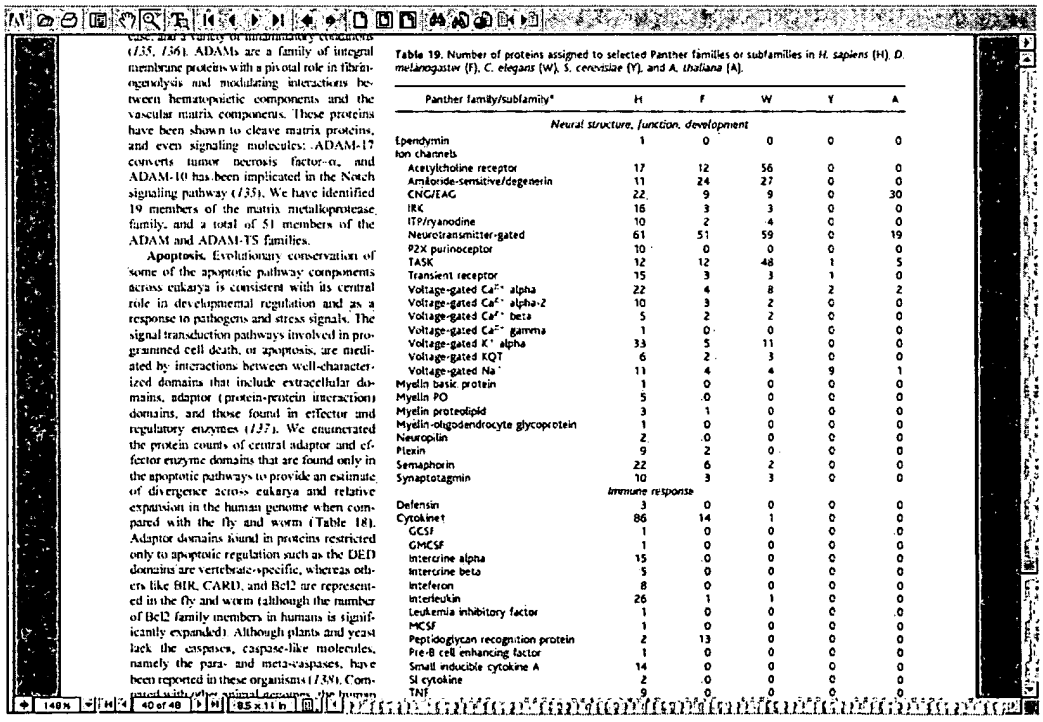


Fig. 8 Cell-cycle regulation of human genes with related biological function. The normalized abundance of mRNA levels, averaged from two experiments, is displayed for each gene. Fluctuation of variance with respect to the mean (units of 0.5, y-axis markers) is shown for 12 consecutive time points, each separated by 2 h (x-axis markers). Results are shown for genes involved in cell cycle control (a–c), nucleosome assembly and DNA replication (d,e), cytoskeletal reorganization (f), apoptosis (g), extracellular matrix remodeling (h) and chromosome segregation (i). The genes shown are as follows: a, CDC2, CDKN3, CDC28, CDC29, ICEKA2, CCNF, and MRGH19. b, CDNB1, CDC20, L2 EF1 and PK4. c, MYT1 and YEET. d, CHAF1B, PCNA, RAD2, replication factors C3 and C4, and LIG1. e, HIT1 and H3. f, STAT, ARF6, MYO5C, MYSL2, SPTN1 and RKOB. g, BAT1, CASP3, SPTAN1 and FLEC1. h, COVEA1, HAS2, ITGA6, NSM, PLAT, PRGT and VASP. i, CEAP6, HRSP, NID, NOSL2, NOSL5, NXSL6, TOP2A and YTB1

Figure - 10



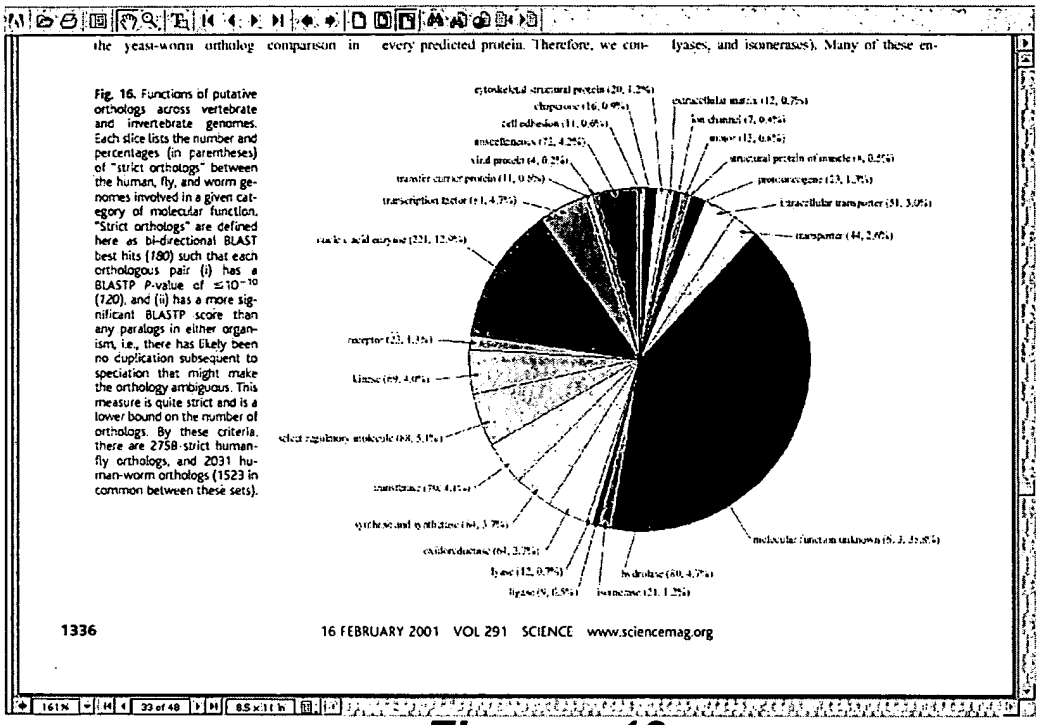
(135, 136). ADAMs are a family of integral membrane proteins with a pivotal role in fibrin-ogenolysis and modulating interactions between hematopoietic components and the vascular matrix components. These proteins have been shown to cleave matrix proteins, and even signaling molecules: ADAM-17 converts tumor necrosis factor-α, and ADAM-10 has been implicated in the Notch signaling pathway (135). We have identified 19 members of the matrix metalloprotease family, and a total of 51 members of the ADAM and ADAM-TS families.

Apoptosis. Evolutionary conservation of some of the apoptotic pathway components across eukarya is consistent with its central role in developmental regulation and as a response to pathogens and stress signals. The signal transduction pathways involved in programmed cell death, or apoptosis, are mediated by interactions between well-characterized domains that include extracellular domains, adaptor (protein-protein interaction) domains, and those found in effector and regulatory enzymes (137). We enumerated the protein counts of central adaptor and effector enzyme domains that are found only in the apoptotic pathways to provide an estimate of divergence across eukarya and relative expansion in the human genome when compared with the fly and worm (Table 18). Adaptor domains found in proteins restricted only to apoptotic regulation such as the DED domains are vertebrate-specific, whereas others like BIR, CARD, and Bcl2 are represented in the fly and worm (although the number of Bcl2 family members in humans is significantly expanded). Although plants and yeast lack the caspases, caspase-like molecules, namely the para- and meta-caspases, have been reported in these organisms (138). Compared with other animal genomes, the human

Table 19. Number of proteins assigned to selected Panther families or subfamilies in *H. sapiens* (H), *D. melanogaster* (F), *C. elegans* (W), *S. cerevisiae* (Y), and *A. thaliana* (A).

Panther family/subfamily*	H	F	W	Y	A
Neural structure, function, development					
Ependymin	1	0	0	0	0
Ion channels					
Acetylcholine receptor	17	12	56	0	0
Amiloride-sensitive/degenerin	11	24	27	0	0
CNG/EAG	22	9	9	0	30
IRK	16	3	3	0	0
ITP/ryanodine	10	2	4	0	0
Neurotransmitter-gated	61	51	59	0	19
P2X purinoceptor	10	0	0	0	0
TASK	12	12	48	1	5
Transient receptor	15	3	3	1	0
Voltage-gated Ca^{2+} alpha	22	4	8	2	2
Voltage-gated Ca^{2+} alpha-2	10	3	2	0	0
Voltage-gated Ca^{2+} beta	5	2	2	0	0
Voltage-gated Ca^{2+} gamma	1	0	0	0	0
Voltage-gated K^+ alpha	33	5	11	0	0
Voltage-gated KQT	6	2	3	0	0
Voltage-gated Na^+	11	4	4	9	1
Myelin basic protein	1	0	0	0	0
Myelin PO	5	0	0	0	0
Myelin proteolipid	3	1	0	0	0
Myelin-oligodendrocyte glycoprotein	1	0	0	0	0
Neuropilin	2	0	0	0	0
Plexin	9	2	0	0	0
Semaphorin	22	6	2	0	0
Synaptotagmin	10	3	3	0	0
Immune response					
Defensin	3	0	0	0	0
Cytokine†	86	14	1	0	0
GCSF	1	0	0	0	0
GMCSF	1	0	0	0	0
Intercrine alpha	15	0	0	0	0
Intercrine beta	5	0	0	0	0
Interferon	8	0	0	0	0
Interleukin	26	1	1	0	0
Leukemia inhibitory factor	1	0	0	0	0
MCSF	1	0	0	0	0
Peptidoglycan recognition protein	2	13	0	0	0
Pre-B cell enhancing factor	1	0	0	0	0
Small inducible cytokine A	14	0	0	0	0
SI cytokine	2	0	0	0	0
TNF	9	0	0	0	0

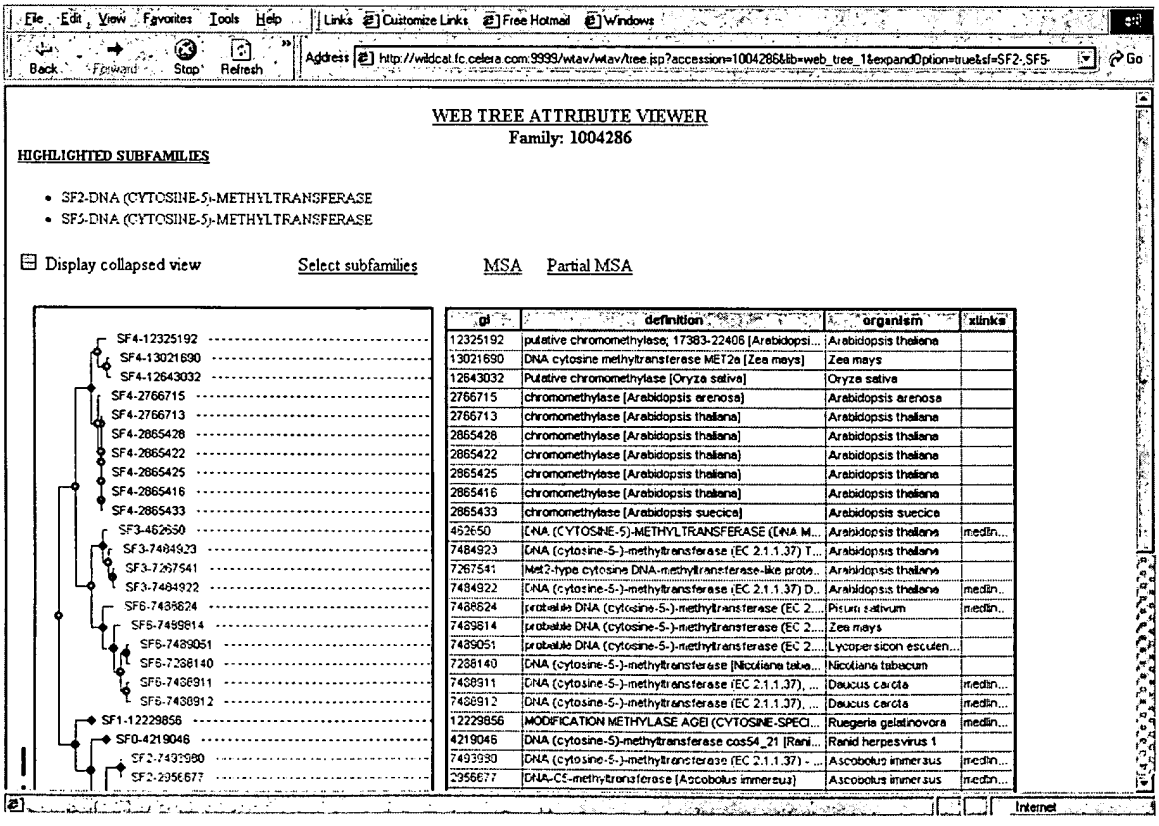
Figure - 11



the yeast-worm ortholog comparison in every predicted protein. Therefore, we con- lyases, and isomerases). Many of these en-

Fig. 16. Functions of putative orthologs across vertebrate and invertebrate genomes. Each slice lists the number and percentages (in parentheses) of "strict orthologs" between the human, fly, and worm genomes involved in a given category of molecular function. "Strict orthologs" are defined here as bi-directional BLAST best hits (*180*) such that each orthologous pair (i) has a BLASTP *P*-value of $\leq 10^{-10}$ (*120*), and (ii) has a more significant BLASTP score than any paralogs in either organism, i.e., there has likely been no duplication subsequent to speciation that might make the orthology ambiguous. This measure is quite strict and is a lower bound on the number of orthologs. By these criteria, there are 2758 strict human-fly orthologs, and 2031 human-worm orthologs (1523 in common between these sets).

Figure - 12



gi	definition	organism	xlinks
12325192	putative chromomethylase; 17383-22406 [Arabidopsi...	Arabidopsis thaliana	
13021690	DNA cytosine methyltransferase MET2a [Zea mays]	Zea mays	
12643032	Putative chromomethylase [Oryza sativa]	Oryza sativa	
2766715	chromomethylase [Arabidopsis arenosa]	Arabidopsis arenosa	
2766713	chromomethylase [Arabidopsis thaliana]	Arabidopsis thaliana	
2865428	chromomethylase [Arabidopsis thaliana]	Arabidopsis thaliana	
2865422	chromomethylase [Arabidopsis thaliana]	Arabidopsis thaliana	
2865425	chromomethylase [Arabidopsis thaliana]	Arabidopsis thaliana	
2865416	chromomethylase [Arabidopsis thaliana]	Arabidopsis thaliana	
2865433	chromomethylase [Arabidopsis suecica]	Arabidopsis suecica	
462650	DNA (CYTOSINE-5)-METHYLTRANSFERASE (DNA M...	Arabidopsis thaliana	medlin...
7484923	DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37) T...	Arabidopsis thaliana	
7267541	Met2-type cytosine DNA-methyltransferase-like prote...	Arabidopsis thaliana	
7484922	DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37) D...	Arabidopsis thaliana	medlin...
7488624	probable DNA (cytosine-5-)-methyltransferase (EC 2....	Pisum sativum	medlin...
7489814	probable DNA (cytosine-5-)-methyltransferase (EC 2....	Zea mays	
7489051	probable DNA (cytosine-5-)-methyltransferase (EC 2....	Lycopersicon esculen...	
7238140	DNA (cytosine-5-)-methyltransferase [Nicotiana tabe...	Nicotiana tabacum	
7436911	DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37), ...	Daucus carota	medlin...
7436912	DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37), ...	Daucus carota	medlin...
12229856	MODIFICATION METHYLASE AGEI (CYTOSINE-SPECI...	Ruegeria gelatinovora	medlin...
4219046	DNA (cytosine-5)-methyltransferase cos54_21 [Rani...	Ranid herpesvirus 1	
7493980	DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37) - ...	Ascobolus immersus	medlin...
2956677	DNA-CS-methyltransferase [Ascobolus immersus]	Ascobolus immersus	medlin...

Figure - 13

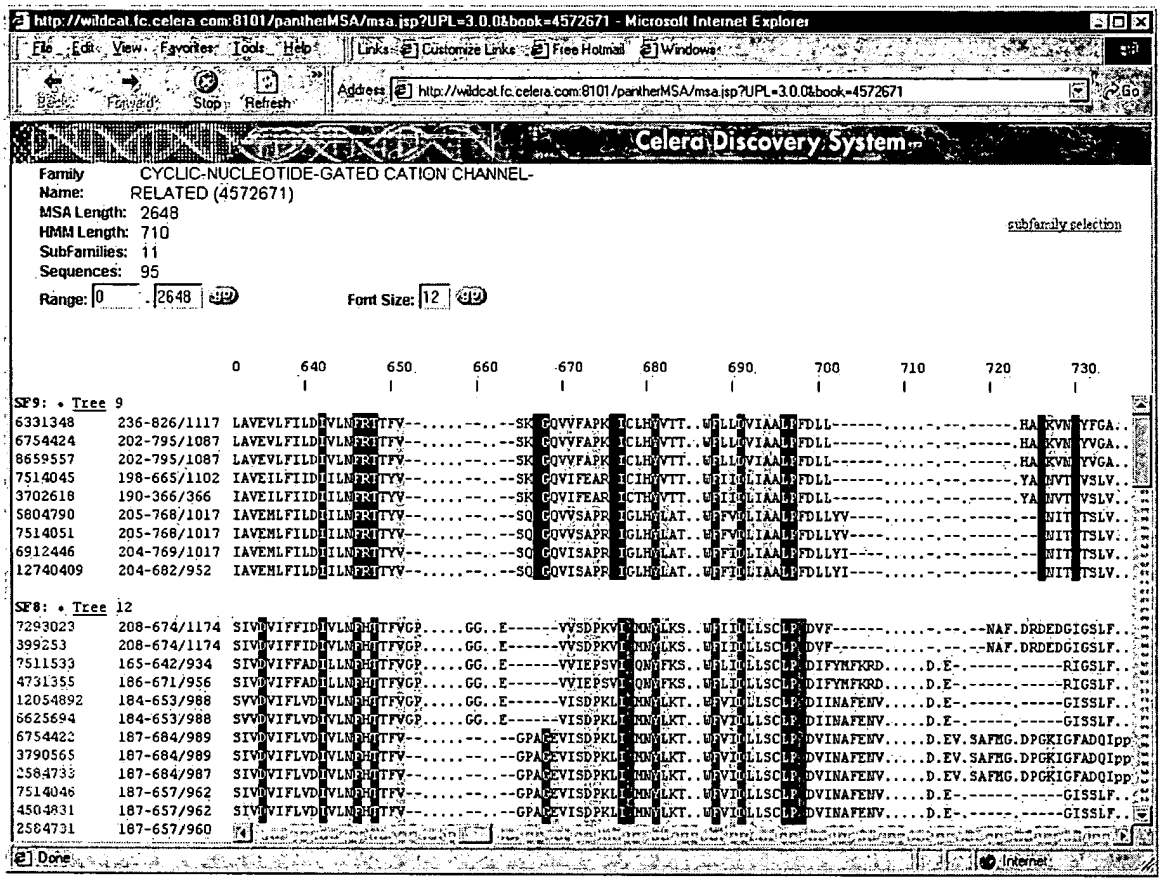


Figure - 14

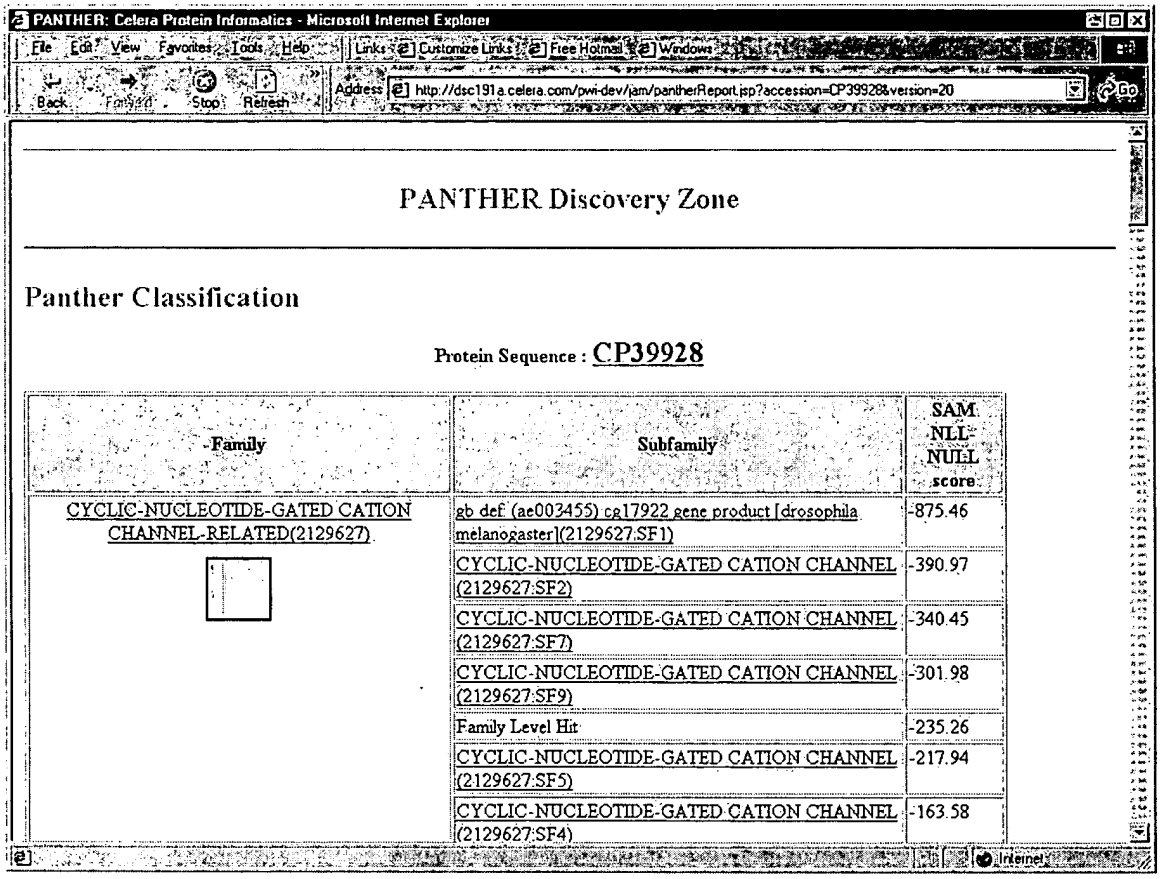

PANTHER: Celera Protein Informatics - Microsoft Internet Explorer
File Edit View Favorites Tools Help
Links Customize Links Free Hotmail Windows
Back Forward Stop Refresh
Address http://dsc191a.celera.com/pwi-dev/jam/pantherReport.jsp?accession=CP39928&version=20
Go
PANTHER Discovery Zone
Panther Classification
Protein Sequence : CP39928
Family
Subfamily
SAM NLL NULL score
CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL-RELATED(2129627)
gb def (ae003455) cg17922 gene product [drosophila melanogaster](2129627:SF1) -875.46
CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL (2129627:SF2) -390.97
CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL (2129627:SF7) -340.45
CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL (2129627:SF9) -301.98
Family Level Hit -235.26
CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL (2129627:SF5) -217.94
CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL (2129627:SF4) -163.58
Internet

Figure - 15

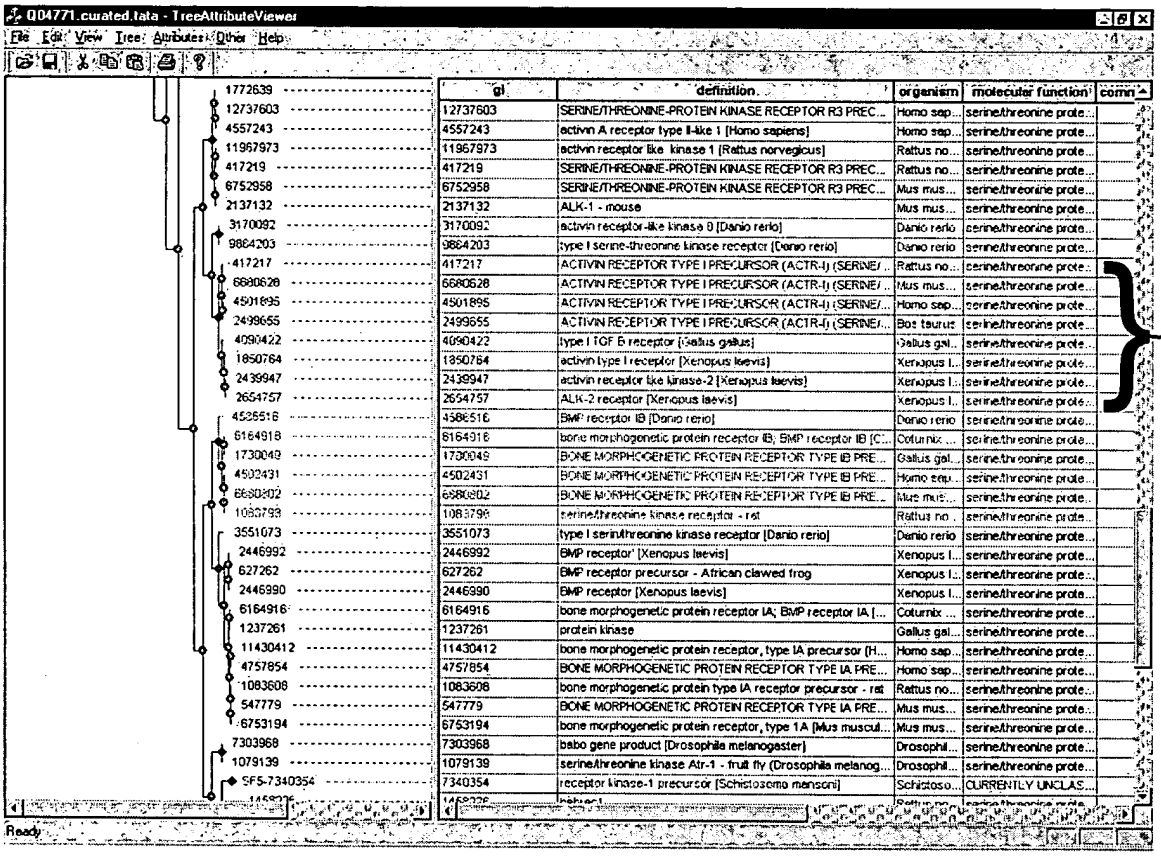

QD4771.curated.tata - TreeAttributeViewer
File Edit View Tree Attributes Other Help
1772639
12737603
4557243
11967973
417219
6752958
2137132
3170092
9864203
417217
6680628
4501895
2499655
4090422
1850764
2439947
2654757
4586516
6164916
1730049
4502431
6680802
1083798
3551073
2446992
627262
2446990
6164916
1237261
11430412
4757854
1083608
547779
6753194
7303968
1079139
SRS-7340354
gi
definition
organism
molecular function
comn
12737603 SERINE/THREONINE-PROTEIN KINASE RECEPTOR R3 PREC... Homo sap... serine/threonine prote...
4557243 activin A receptor type II-like 1 [Homo sapiens] Homo sap... serine/threonine prote...
11967973 activin receptor like kinase 1 [Rattus norvegicus] Rattus no... serine/threonine prote...
417219 SERINE/THREONINE-PROTEIN KINASE RECEPTOR R3 PREC... Rattus no... serine/threonine prote...
6752958 SERINE/THREONINE-PROTEIN KINASE RECEPTOR R3 PREC... Mus mus... serine/threonine prote...
2137132 ALK-1 - mouse Mus mus... serine/threonine prote...
3170092 activin receptor-like kinase 8 [Danio rerio] Danio rerio serine/threonine prote...
9864203 type I serine-threonine kinase receptor [Danio rerio] Danio rerio serine/threonine prote...
417217 ACTIVIN RECEPTOR TYPE I PRECURSOR (ACTR-I) (SERINE/... Rattus no... serine/threonine prote...
6680628 ACTIVIN RECEPTOR TYPE I PRECURSOR (ACTR-I) (SERINE/... Mus mus... serine/threonine prote...
4501895 ACTIVIN RECEPTOR TYPE I PRECURSOR (ACTR-I) (SERINE/... Homo sap... serine/threonine prote...
2499655 ACTIVIN RECEPTOR TYPE I PRECURSOR (ACTR-I) (SERINE/... Bos taurus serine/threonine prote...
4090422 type I TGF-B receptor [Gallus gallus] Gallus gal... serine/threonine prote...
1850764 activin type I receptor [Xenopus laevis] Xenopus l... serine/threonine prote...
2439947 activin receptor like kinase-2 [Xenopus laevis] Xenopus l... serine/threonine prote...
2654757 ALK-2 receptor [Xenopus laevis] Xenopus l... serine/threonine prote...
4586516 BMP receptor IB [Danio rerio] Danio rerio serine/threonine prote...
6164916 bone morphogenetic protein receptor IB; BMP receptor IB [C... Coturnix ... serine/threonine prote...
1730049 BONE MORPHOGENETIC PROTEIN RECEPTOR TYPE IB PRE... Gallus gal... serine/threonine prote...
4502431 BONE MORPHOGENETIC PROTEIN RECEPTOR TYPE IB PRE... Homo sap... serine/threonine prote...
6680802 BONE MORPHOGENETIC PROTEIN RECEPTOR TYPE IB PRE... Mus mus... serine/threonine prote...
1083798 serine/threonine kinase receptor - rat Rattus no... serine/threonine prote...
3551073 type I serin/threonine kinase receptor [Danio rerio] Danio rerio serine/threonine prote...
2446992 BMP receptor [Xenopus laevis] Xenopus l... serine/threonine prote...
627262 BMP receptor precursor - African clawed frog Xenopus l... serine/threonine prote...
2446990 BMP receptor [Xenopus laevis] Xenopus l... serine/threonine prote...
6164916 bone morphogenetic protein receptor IA; BMP receptor IA [... Coturnix ... serine/threonine prote...
1237261 protein kinase Gallus gal... serine/threonine prote...
11430412 bone morphogenetic protein receptor, type IA precursor (H... Homo sap... serine/threonine prote...
4757854 BONE MORPHOGENETIC PROTEIN RECEPTOR TYPE IA PRE... Homo sap... serine/threonine prote...
1083608 bone morphogenetic protein type IA receptor precursor - rat Rattus no... serine/threonine prote...
547779 BONE MORPHOGENETIC PROTEIN RECEPTOR TYPE IA PRE... Mus mus... serine/threonine prote...
6753194 bone morphogenetic protein receptor, type 1A [Mus musculi... Mus mus... serine/threonine prote...
7303968 babo gene product [Drosophila melanogaster] Drosophil... serine/threonine prote...
1079139 serine/threonine kinase Atr-1 - fruit fly (Drosophila melanog... Drosophil... serine/threonine prote...
7340354 receptor kinase-1 precursor [Schistosoma mansoni] Schistoso... CURRENTLY UNCLAS...
Ready
100

Figure - 16

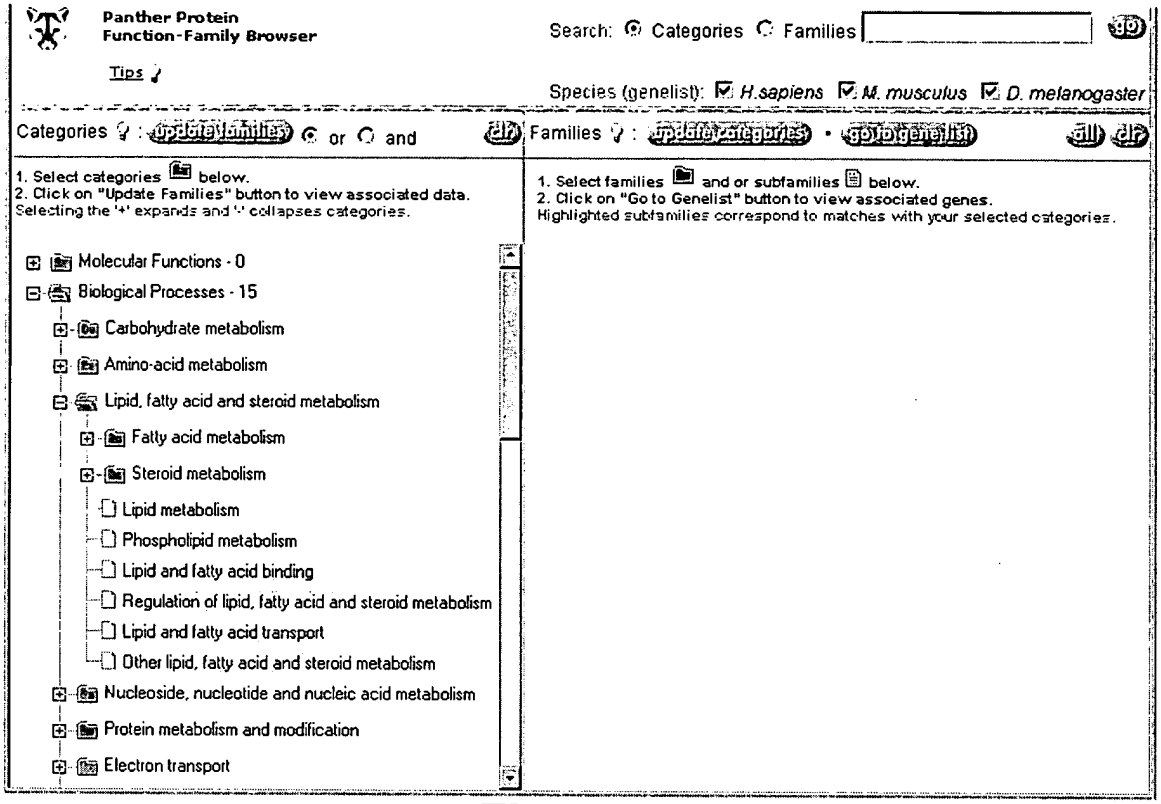


Figure - 17

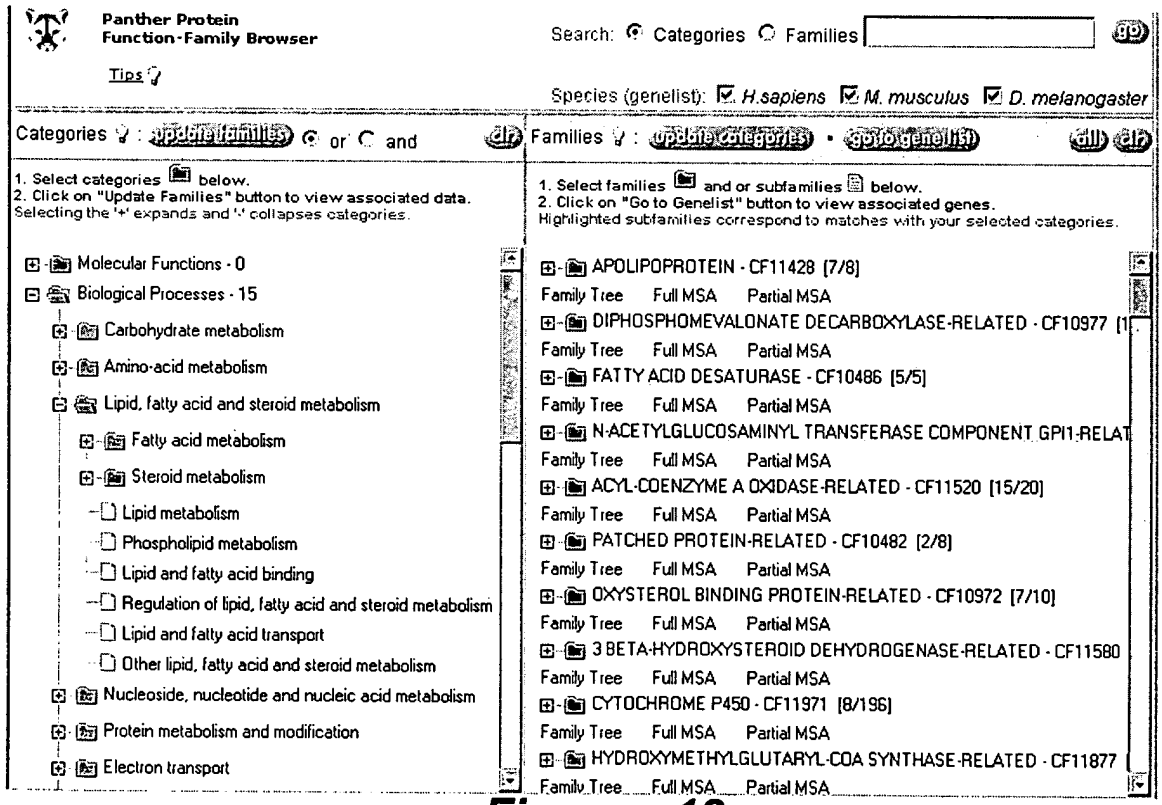


Figure - 18

Function-Family Browser : Panther Gene List HMM Score Cutoff (<): -35.0 Display: 30 update · export

• Sort results by selecting column title. Columns will sort in descending or ascending order.

	ID - Protein	Panther Best Hit • Panther ID family (CF#) or subfamily (SF#)	Panther Score	Relation	Species
345.	gene1	ORPHAN NUCLEAR HORMONE RECEPTOR LRH (CF11154:SF208)	-641.6	●●●	*H sapiens*
346.	gene2	ORPHAN NUCLEAR HORMONE RECEPTOR LRH (CF11154:SF208)	-641.51	●●●	*H sapiens*
347.	gene3	RETINOIC ACID RECEPTOR RXR-ALPHA (CF11154:SF216)	-670.15	●●●	*H sapiens*
348.	gene4	RETINOIC ACID RECEPTOR RXR-GAMMA (CF11154:SF217)	-623.86	●●●	*H sapiens*
349.	gene5	RETINOIC ACID RECEPTOR RXR-BETA (CF11154:SF218)	-611.24	●●●	*H sapiens*
350.	gene6	PHOSPHOLIPASE D1 (CF11198:SF4)	-2100.67	●●●	*H sapiens*
351.	gene7	PHOSPHOLIPASE D2 (CF11198:SF5)	-2047.31	●●●	*H sapiens*
352.	gene8	INOSITOL PHOSPHATASE SKIP (CF11200:SF21)	-361.22	●●●	*H sapiens*
353.	gene9	INOSITOL PHOSPHATASE SKIP (CF11200:SF21)	-343.71	●●●	*H sapiens*
354.	gene10	INOSITOL PHOSPHATASE SKIP-RELATED (CF11200:SF22)	-389.15	●●●	*D. melanogaster*
355.	gene11	INOSITOL PHOSPHATASE SKIP-RELATED (CF11200:SF22)	-354.86	●●●	*D. melanogaster*
356.	gene12	SPHINGOSINE PHOSPHATE LYASE-RELATED (CF11253:SF10)	-722.67	●●●	*D. melanogaster*
357.	gene13	SPHINGOSINE PHOSPHATE LYASE-RELATED (CF11253:SF10)	-722.67	●●●	*D. melanogaster*
358.	gene14	SPHINGOSINE PHOSPHATE LYASE-RELATED (CF11253:SF10)	-697.26	●●●	*H sapiens*
359.	gene15	DIACYLGLYCEROL KINASE, EPSILON (CF11255:SF12)	-997.86	●●●	*H sapiens*

Figure - 19

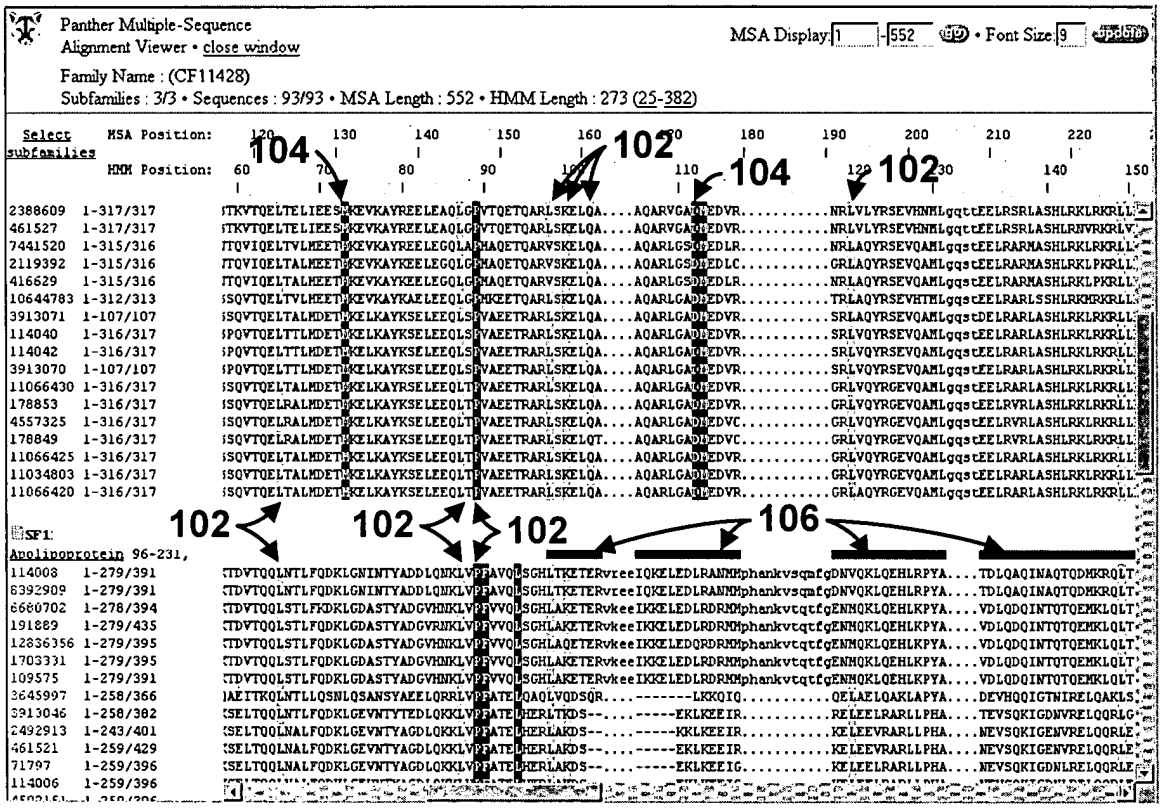

Panther Multiple-Sequence
Alignment Viewer • close window
MSA Display: 1 -552 • Font Size: 9
Family Name : (CF11428)
Subfamilies : 3/3 • Sequences : 93/93 • MSA Length : 552 • HMM Length : 273 (25-382)
Select subfamilies
MSA Position:
HMM Position:
104
102
104
102
102
102
102
106
SF1:
Apolipoprotein 96-231,

Figure - 20

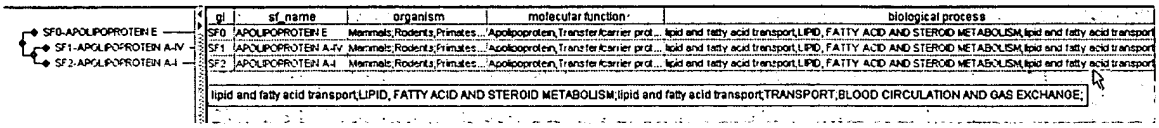
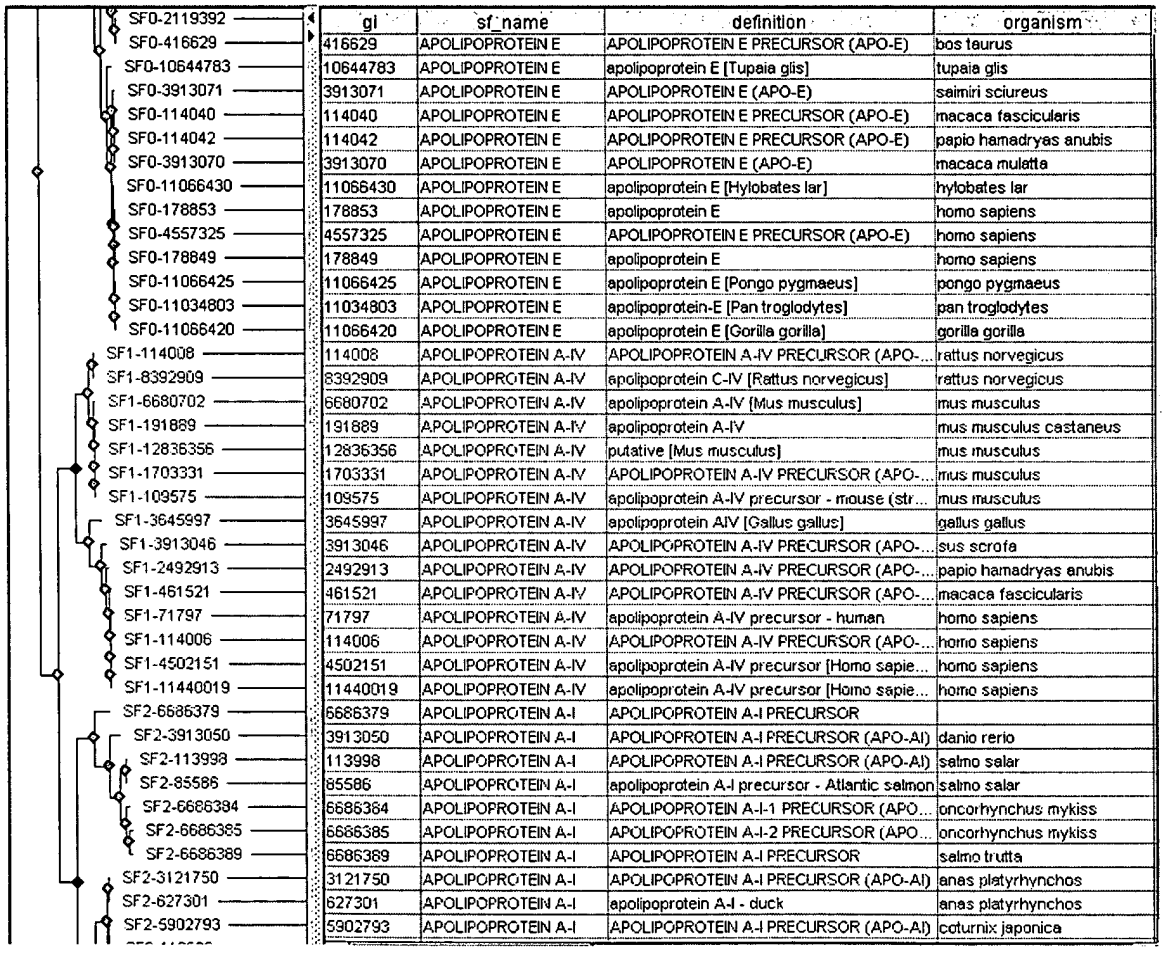


Figure - 21A



gi	sf_name	definition	organism
416629	APOLIPOPROTEIN E	APOLIPOPROTEIN E PRECURSOR (APO-E)	bos taurus
10644783	APOLIPOPROTEIN E	apolipoprotein E [Tupaia glis]	tupaia glis
3913071	APOLIPOPROTEIN E	APOLIPOPROTEIN E (APO-E)	saimiri sciureus
114040	APOLIPOPROTEIN E	APOLIPOPROTEIN E PRECURSOR (APO-E)	macaca fascicularis
114042	APOLIPOPROTEIN E	APOLIPOPROTEIN E PRECURSOR (APO-E)	papio hamadryas anubis
3913070	APOLIPOPROTEIN E	APOLIPOPROTEIN E (APO-E)	macaca mulatta
11066430	APOLIPOPROTEIN E	apolipoprotein E [Hylobates lar]	hylobates lar
178853	APOLIPOPROTEIN E	apolipoprotein E	homo sapiens
4557325	APOLIPOPROTEIN E	APOLIPOPROTEIN E PRECURSOR (APO-E)	homo sapiens
178849	APOLIPOPROTEIN E	apolipoprotein E	homo sapiens
11066425	APOLIPOPROTEIN E	apolipoprotein E [Pongo pygmaeus]	pongo pygmaeus
11034803	APOLIPOPROTEIN E	apolipoprotein-E [Pan troglodytes]	pan troglodytes
11066420	APOLIPOPROTEIN E	apolipoprotein E [Gorilla gorilla]	gorilla gorilla
114008	APOLIPOPROTEIN A-IV	APOLIPOPROTEIN A-IV PRECURSOR (APO-...	rattus norvegicus
8392909	APOLIPOPROTEIN A-IV	apolipoprotein C-IV [Rattus norvegicus]	rattus norvegicus
6680702	APOLIPOPROTEIN A-IV	apolipoprotein A-IV [Mus musculus]	mus musculus
191889	APOLIPOPROTEIN A-IV	apolipoprotein A-IV	mus musculus castaneus
12836356	APOLIPOPROTEIN A-IV	putative [Mus musculus]	mus musculus
1703331	APOLIPOPROTEIN A-IV	APOLIPOPROTEIN A-IV PRECURSOR (APO-...	mus musculus
109575	APOLIPOPROTEIN A-IV	apolipoprotein A-IV precursor - mouse (str...	mus musculus
3645997	APOLIPOPROTEIN A-IV	apolipoprotein AIV [Gallus gallus]	gallus gallus
3913046	APOLIPOPROTEIN A-IV	APOLIPOPROTEIN A-IV PRECURSOR (APO-...	sus scrofa
2492913	APOLIPOPROTEIN A-IV	APOLIPOPROTEIN A-IV PRECURSOR (APO-...	papio hamadryas anubis
461521	APOLIPOPROTEIN A-IV	APOLIPOPROTEIN A-IV PRECURSOR (APO-...	macaca fascicularis
71797	APOLIPOPROTEIN A-IV	apolipoprotein A-IV precursor - human	homo sapiens
114006	APOLIPOPROTEIN A-IV	APOLIPOPROTEIN A-IV PRECURSOR (APO-...	homo sapiens
4502151	APOLIPOPROTEIN A-IV	apolipoprotein A-IV precursor [Homo sapie...	homo sapiens
11440019	APOLIPOPROTEIN A-IV	apolipoprotein A-IV precursor [Homo sapie...	homo sapiens
6686379	APOLIPOPROTEIN A-I	APOLIPOPROTEIN A-I PRECURSOR	
3913050	APOLIPOPROTEIN A-I	APOLIPOPROTEIN A-I PRECURSOR (APO-AI)	danio rerio
113998	APOLIPOPROTEIN A-I	APOLIPOPROTEIN A-I PRECURSOR (APO-AI)	salmo salar
85586	APOLIPOPROTEIN A-I	apolipoprotein A-I precursor - Atlantic salmon	salmo salar
6686384	APOLIPOPROTEIN A-I	APOLIPOPROTEIN A-I-1 PRECURSOR (APO...	oncorhynchus mykiss
6686385	APOLIPOPROTEIN A-I	APOLIPOPROTEIN A-I-2 PRECURSOR (APO...	oncorhynchus mykiss
6686389	APOLIPOPROTEIN A-I	APOLIPOPROTEIN A-I PRECURSOR	salmo trutta
3121750	APOLIPOPROTEIN A-I	APOLIPOPROTEIN A-I PRECURSOR (APO-AI)	anas platyrhynchos
627301	APOLIPOPROTEIN A-I	apolipoprotein A-I - duck	anas platyrhynchos
5902793	APOLIPOPROTEIN A-I	APOLIPOPROTEIN A-I PRECURSOR (APO-AI)	coturnix japonica

Figure - 21B

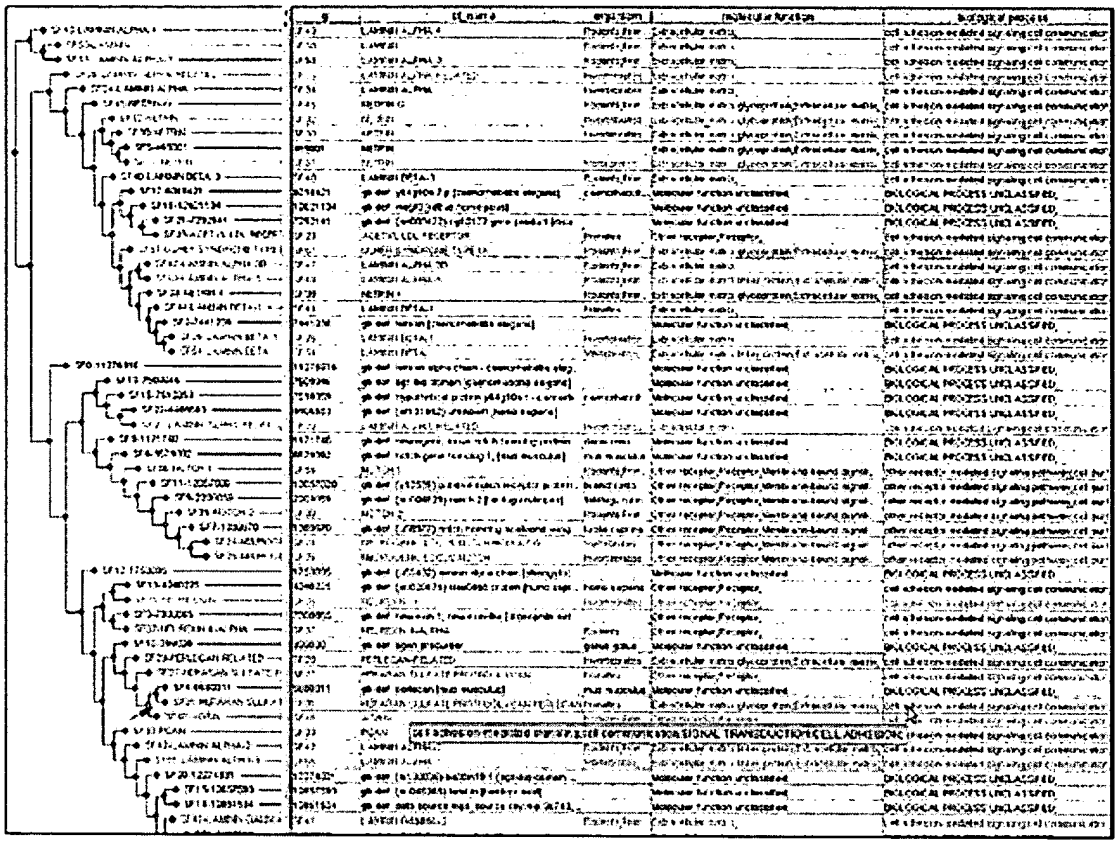


Figure - 22A

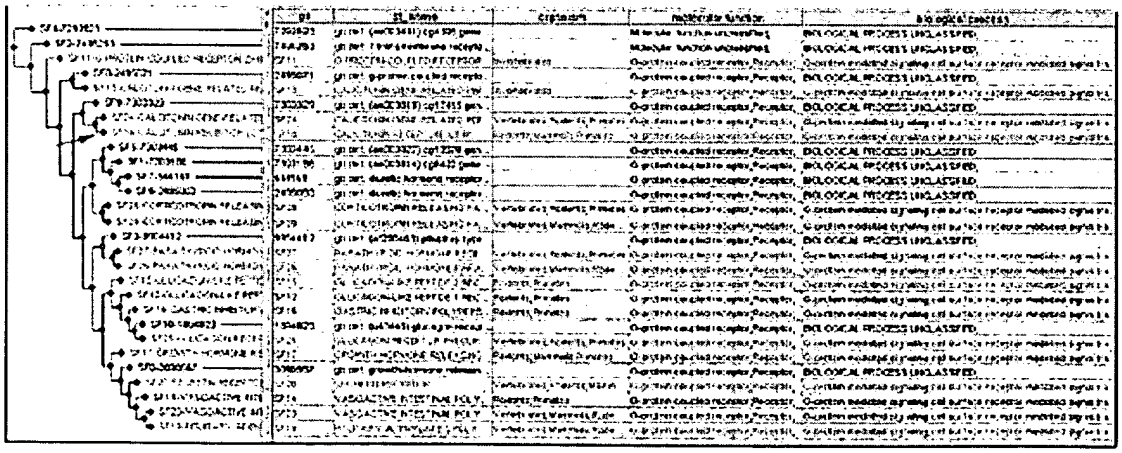


Figure - 22B

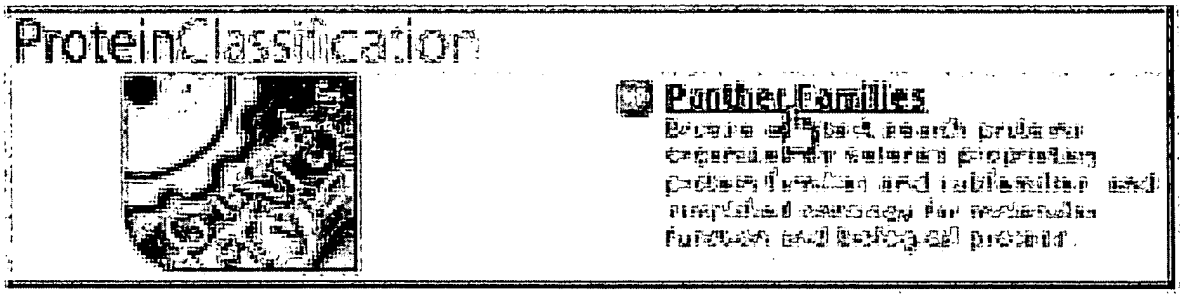


Figure - 23

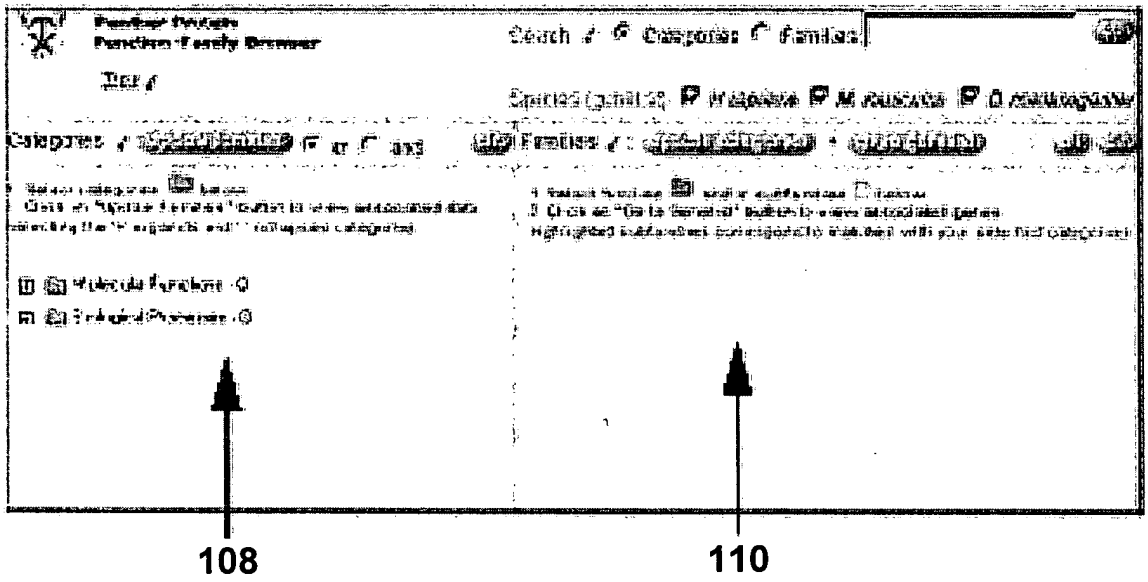


Figure - 24

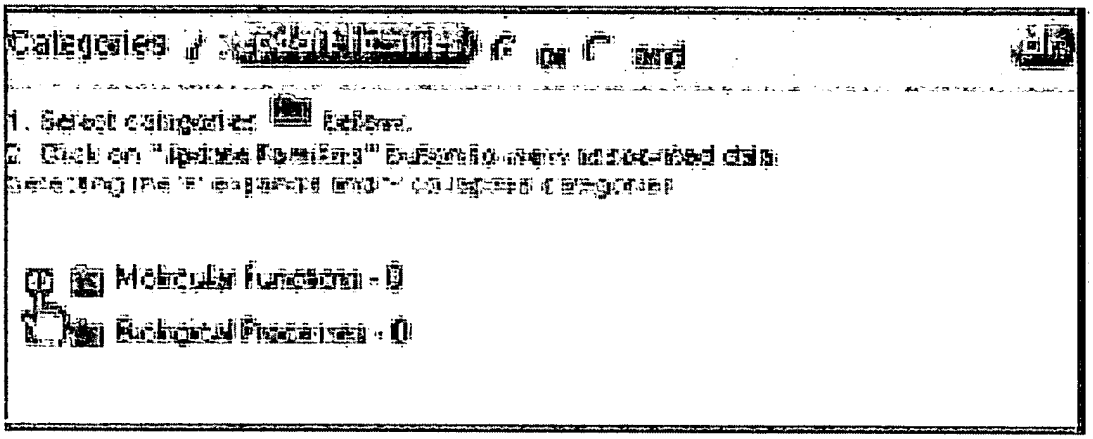


Figure - 25

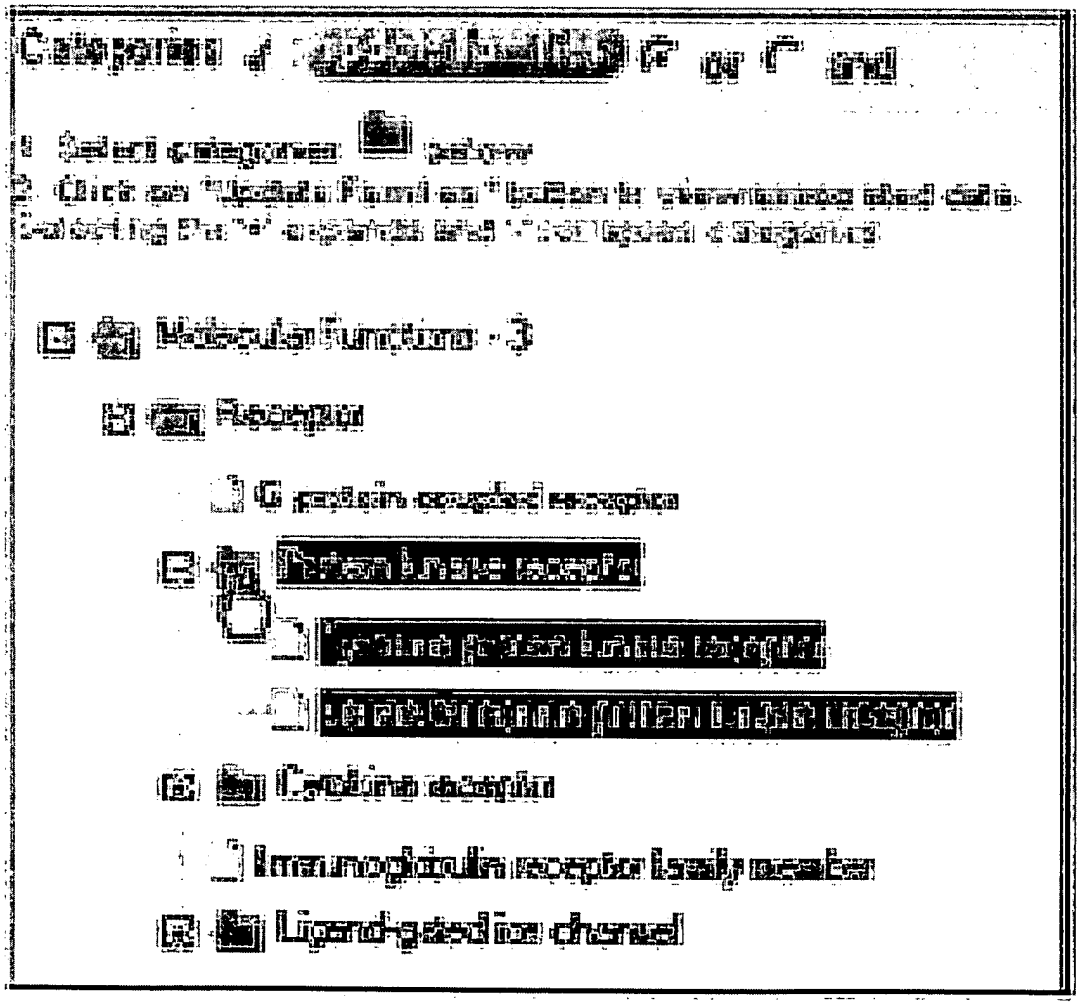


Figure - 26

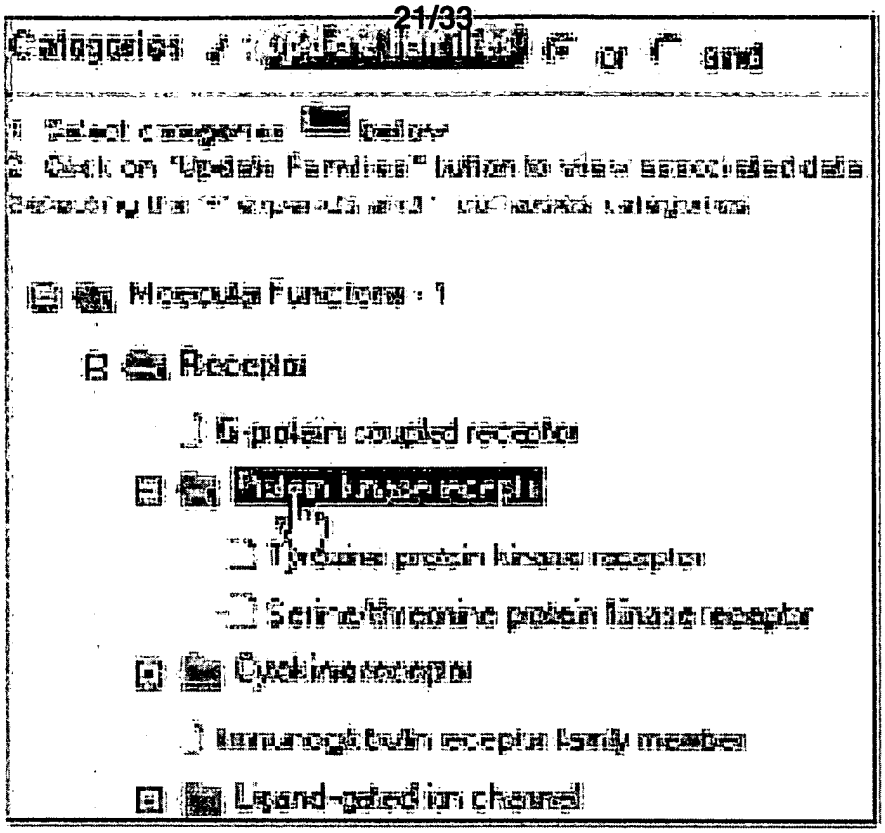


Figure - 27

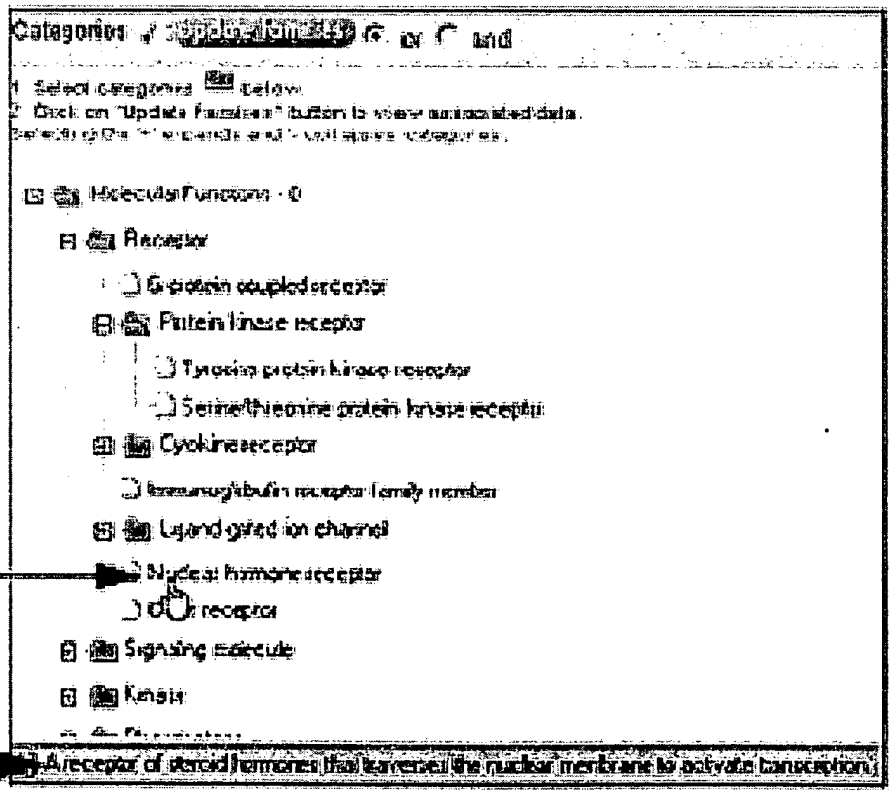


Figure - 28

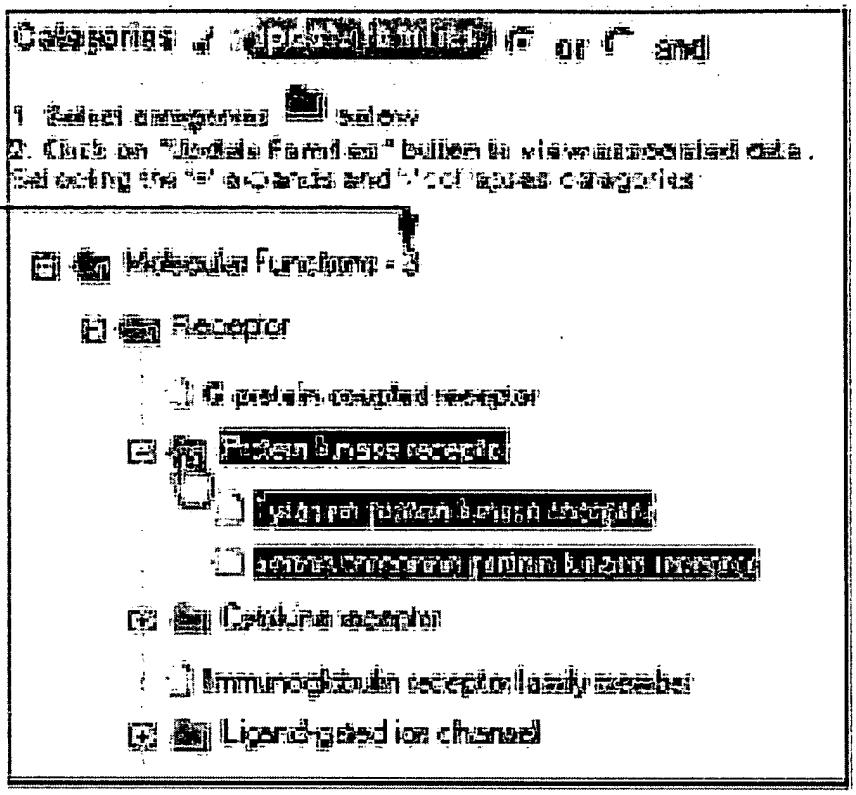


Figure - 29

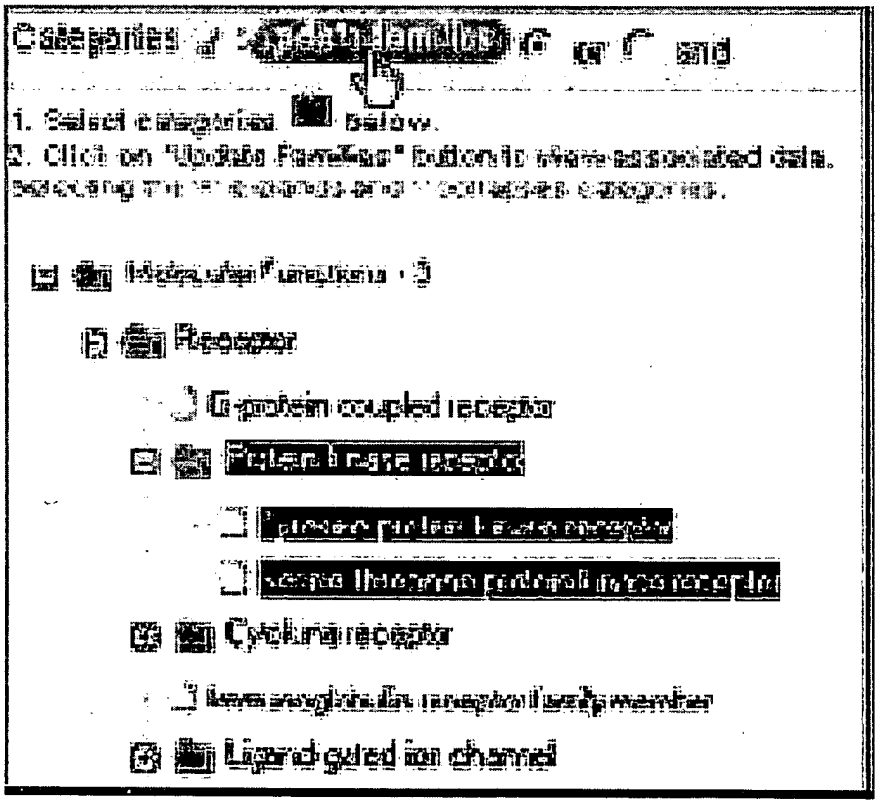


Figure - 30

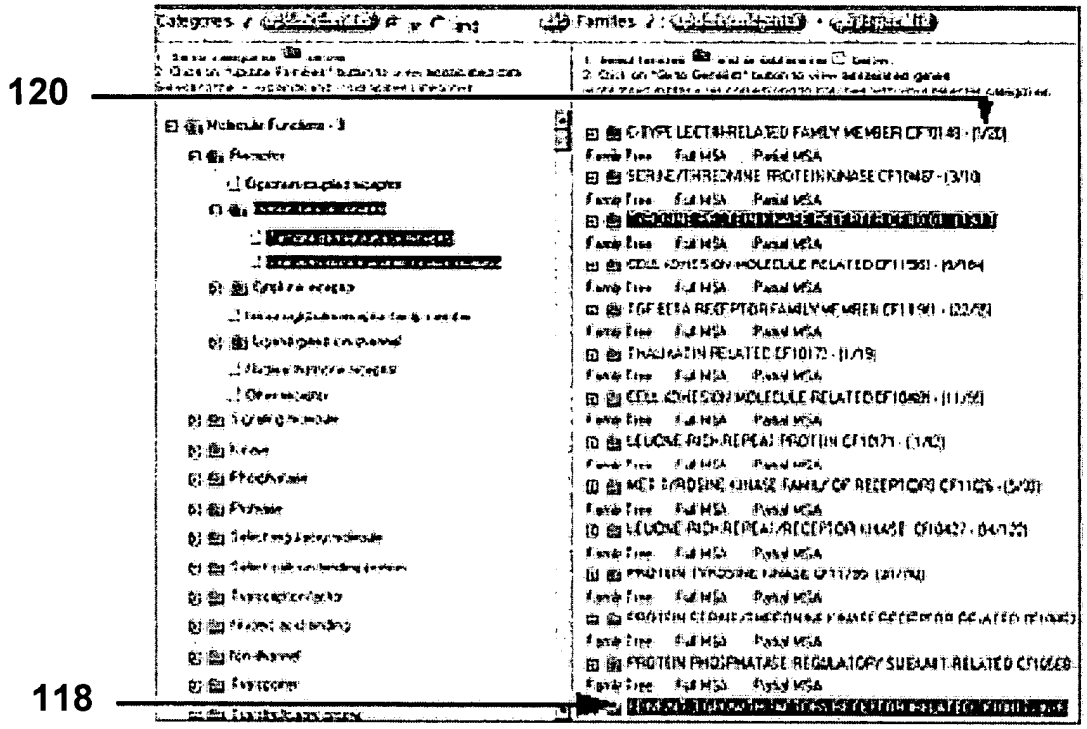


Figure - 31

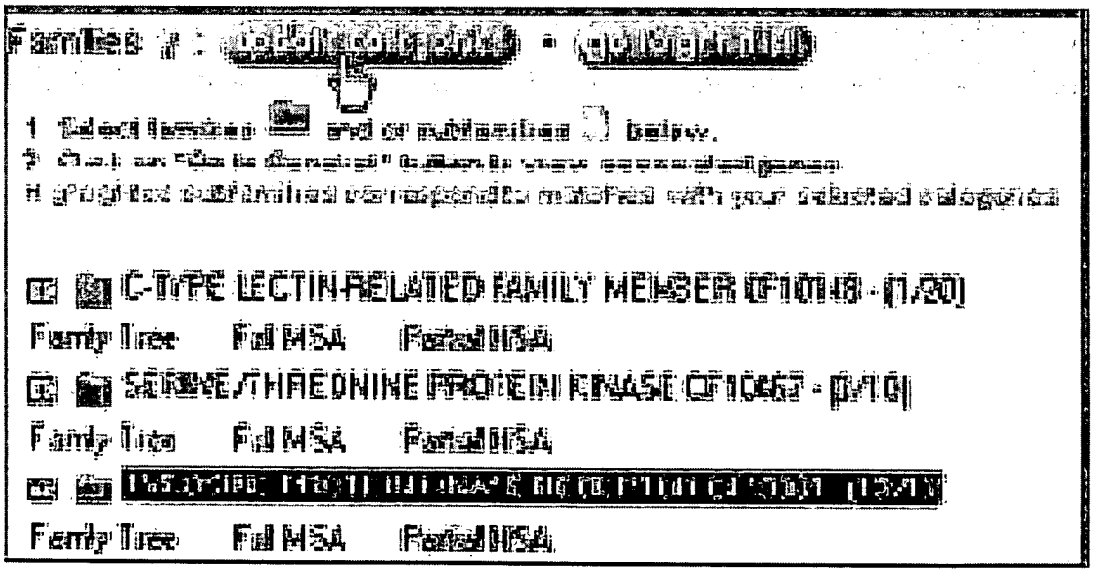


Figure - 32

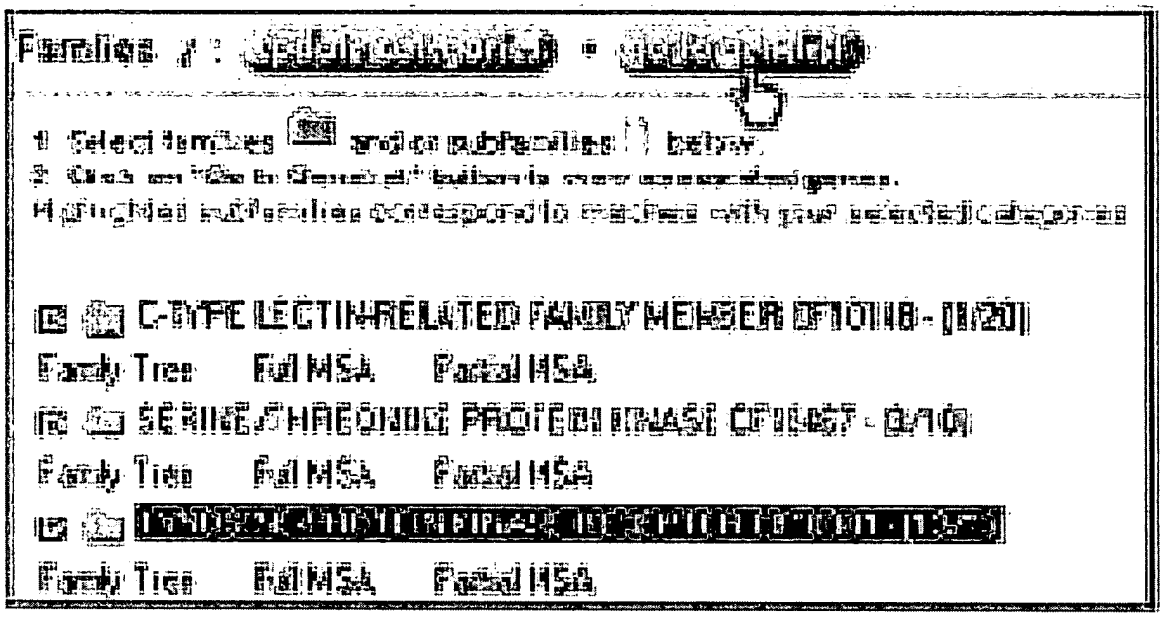


Figure - 33

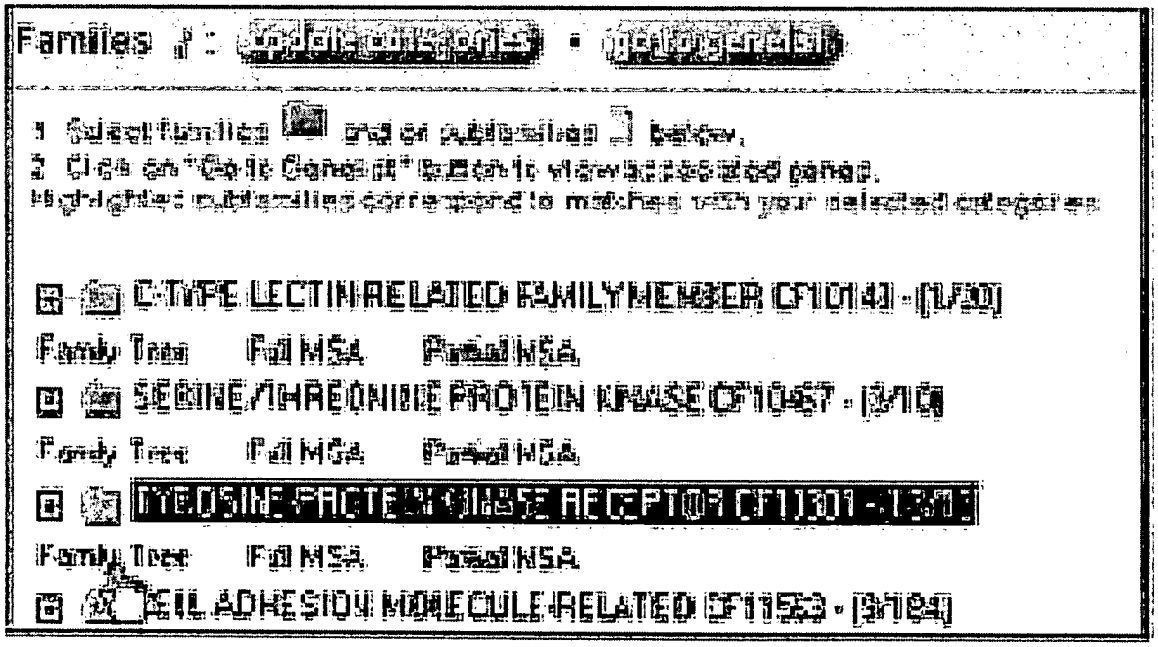


Figure - 34

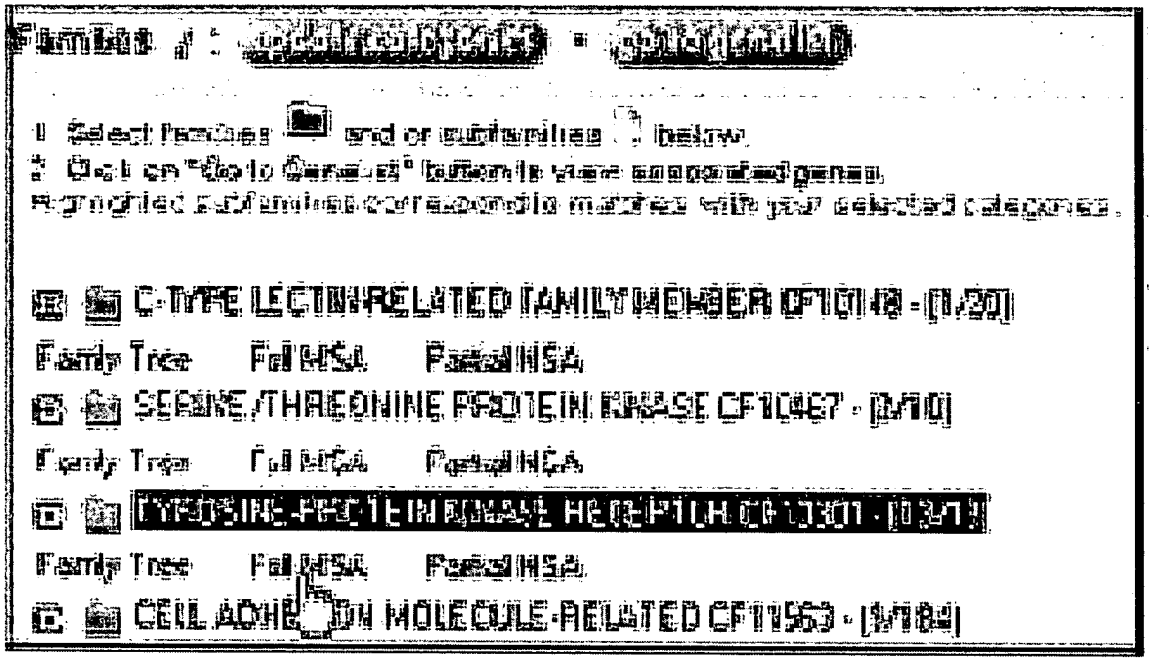


Figure - 35

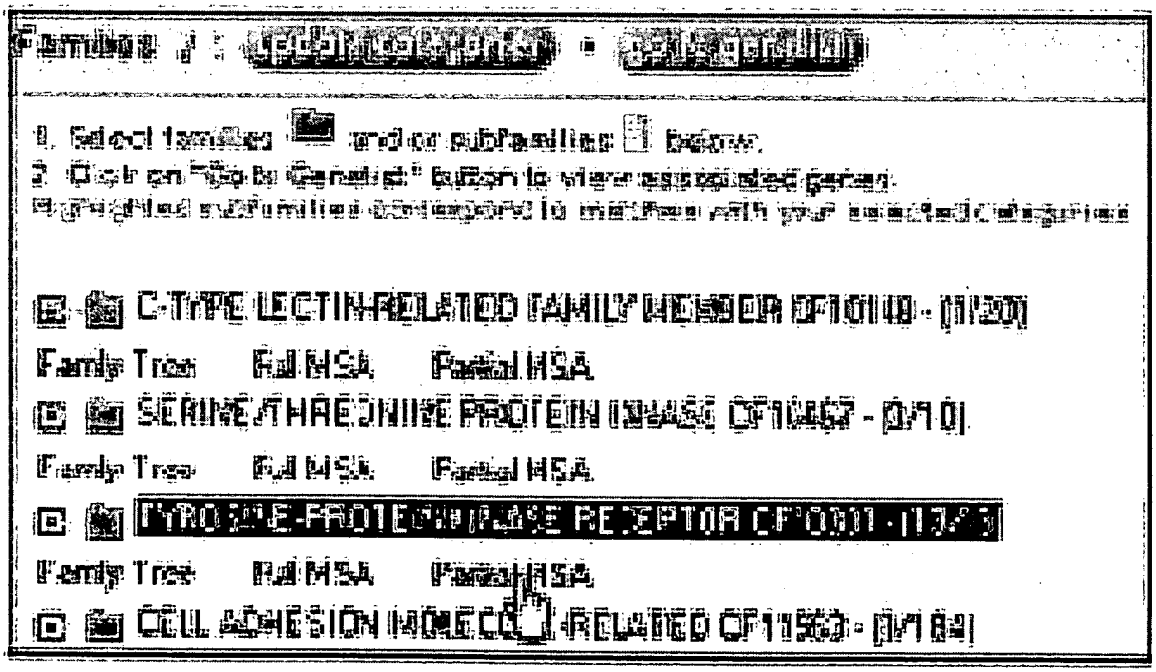


Figure - 36

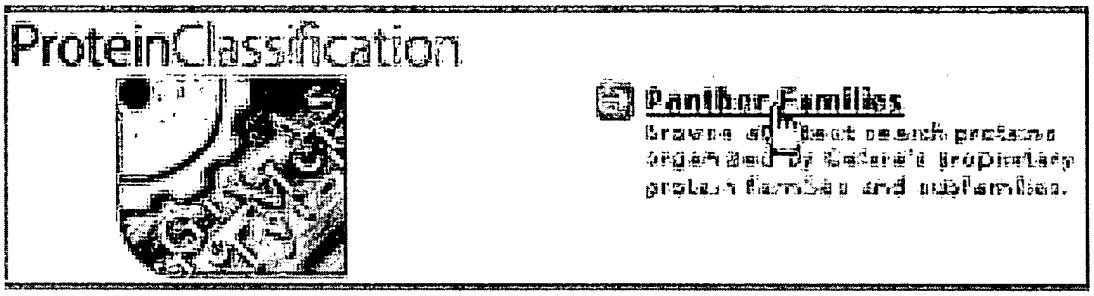


Figure - 37

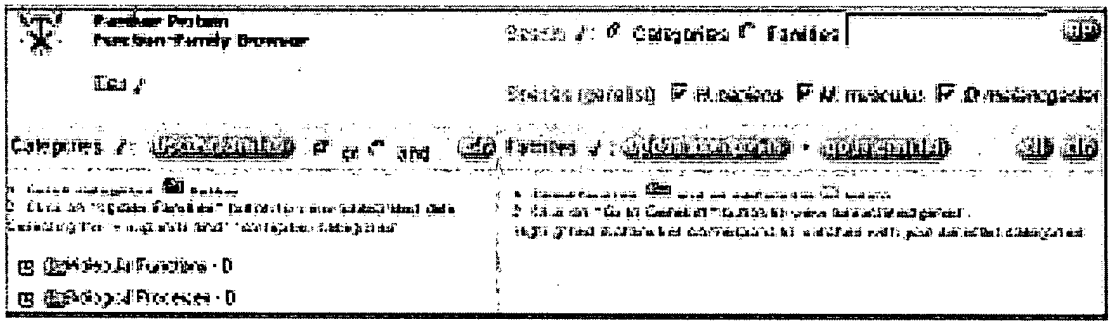


Figure - 38

Figure - 39

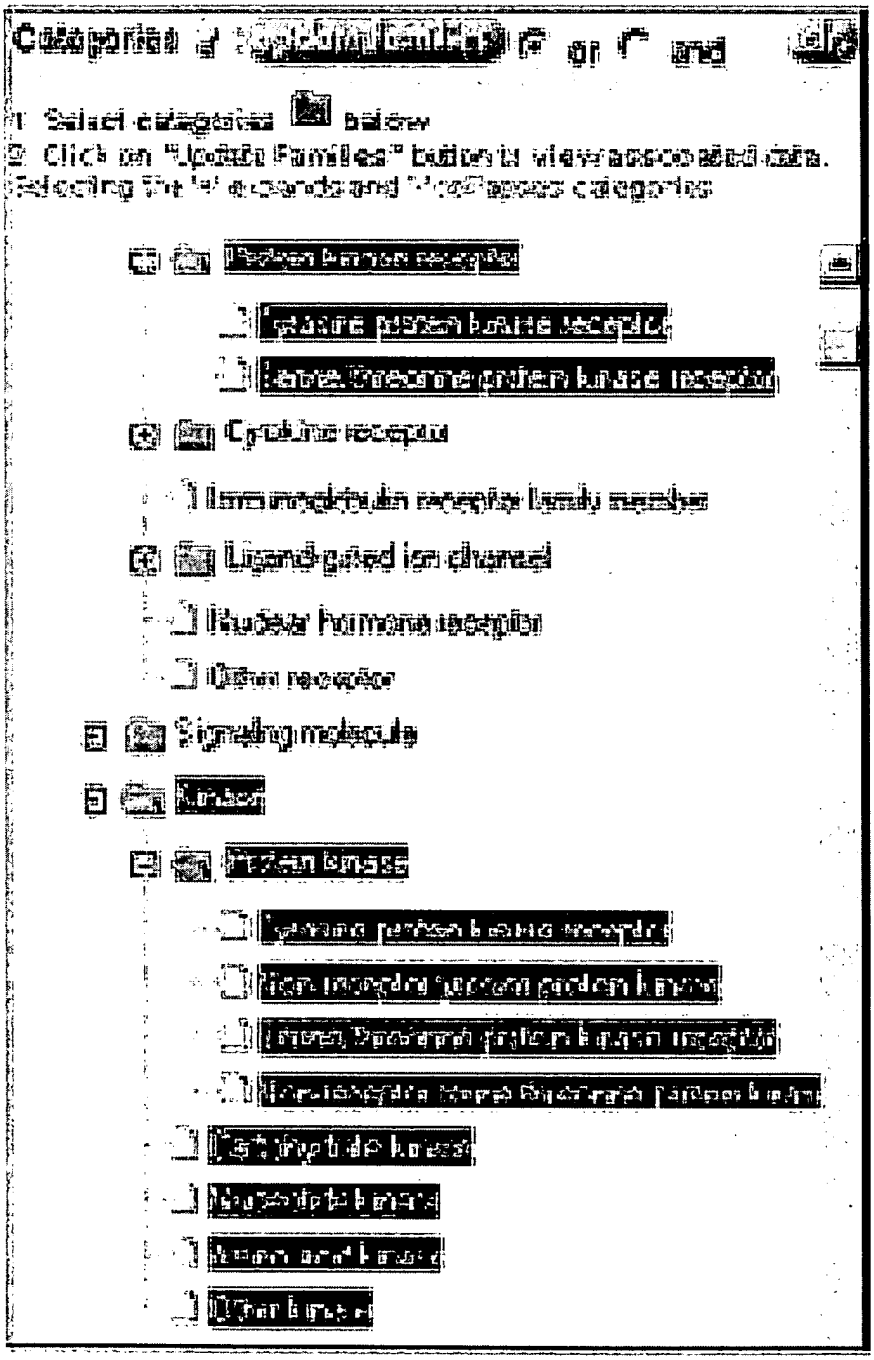


Figure - 40

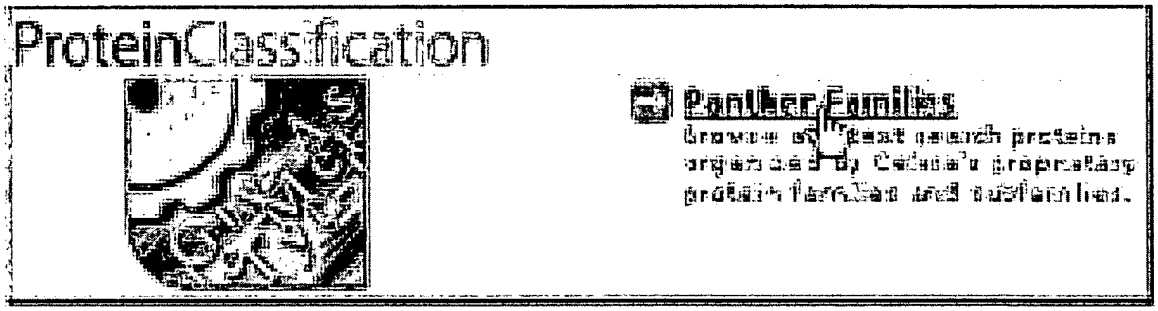


Figure - 41

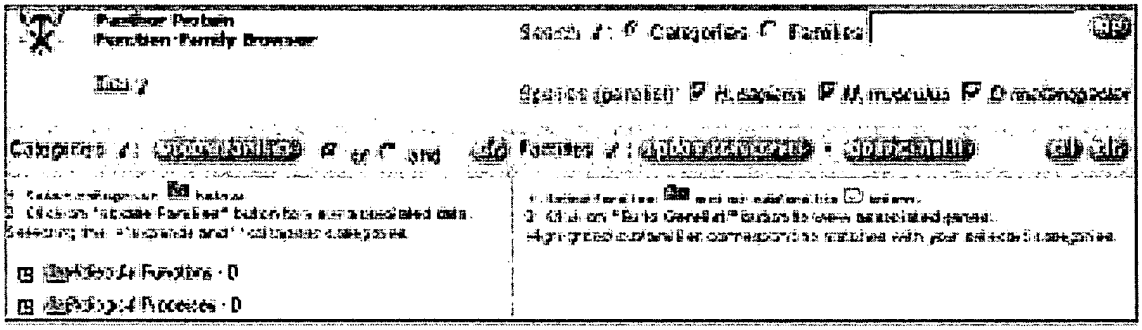


Figure - 42

Figure - 43

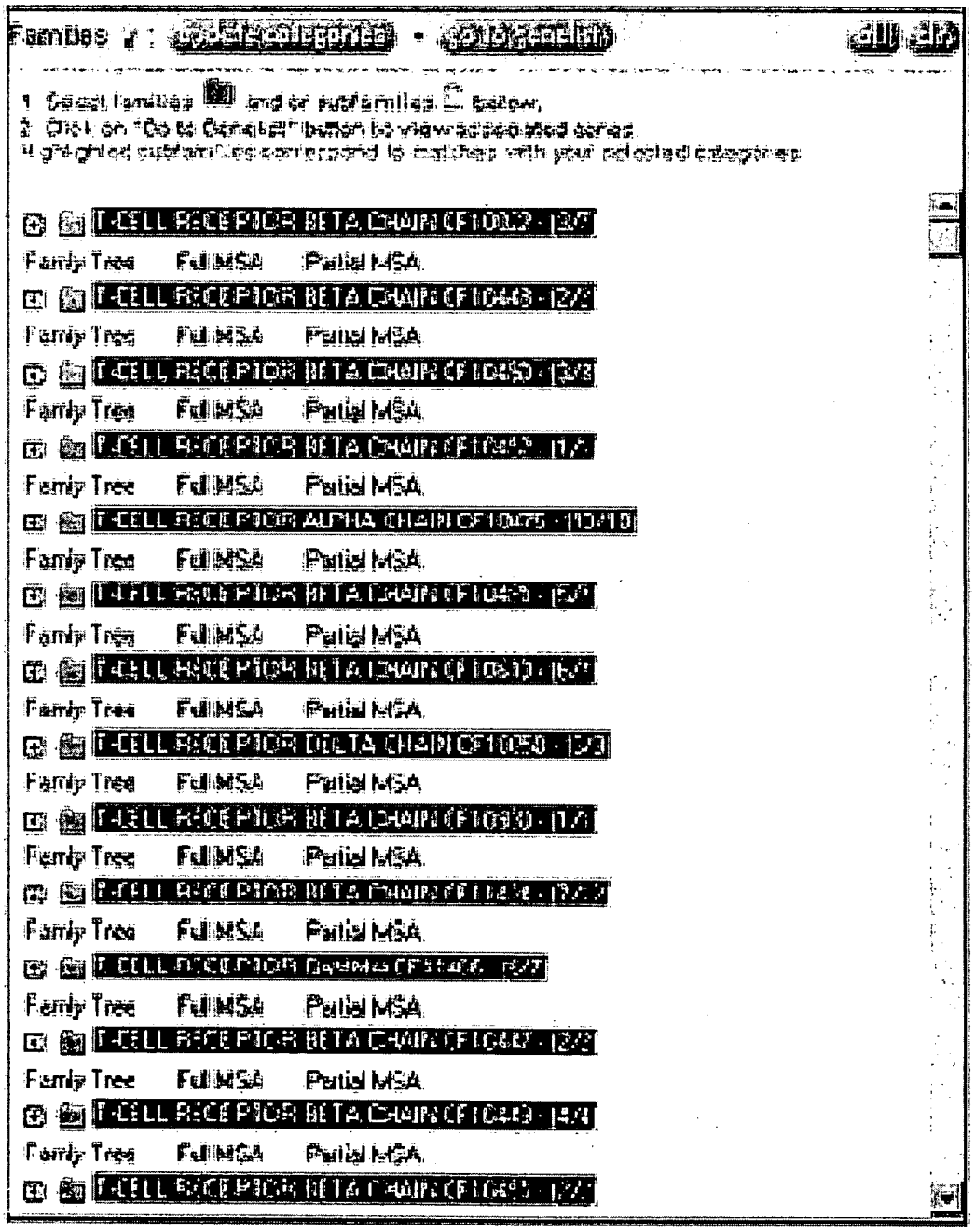


Figure - 44

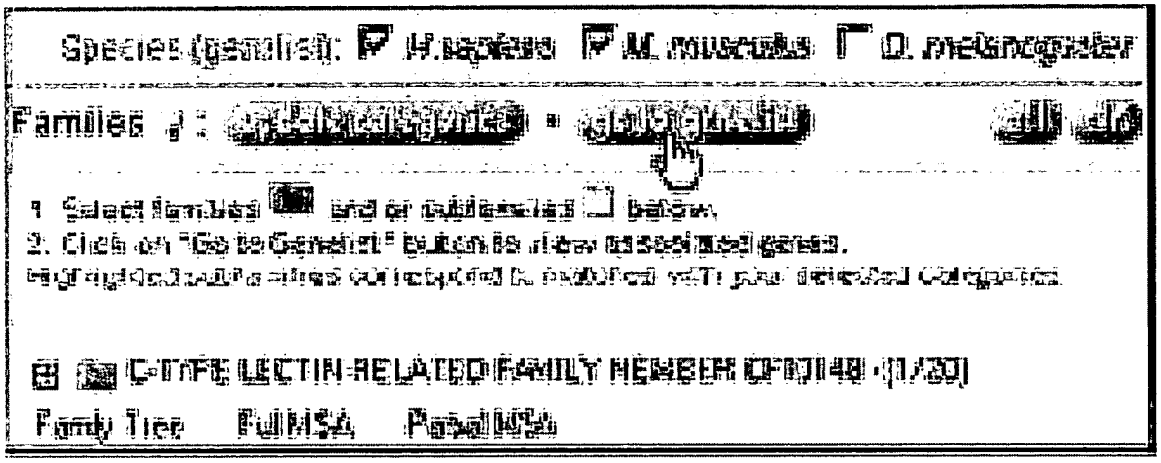


Figure - 45

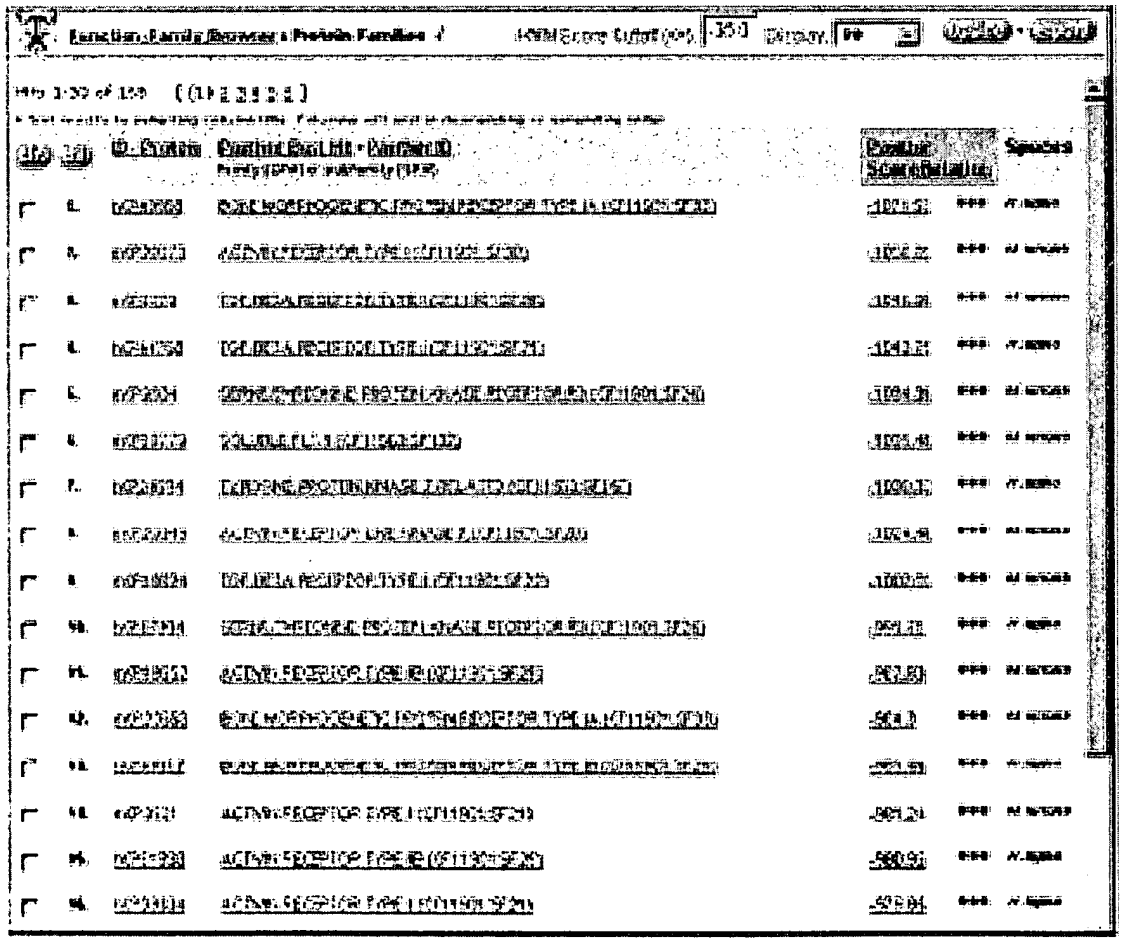


Figure - 46

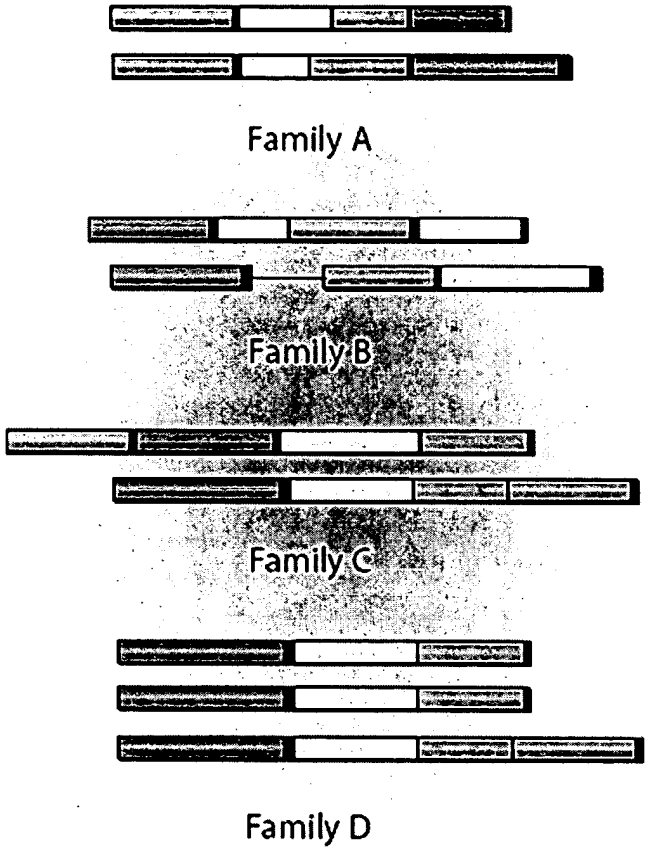


Figure - 47

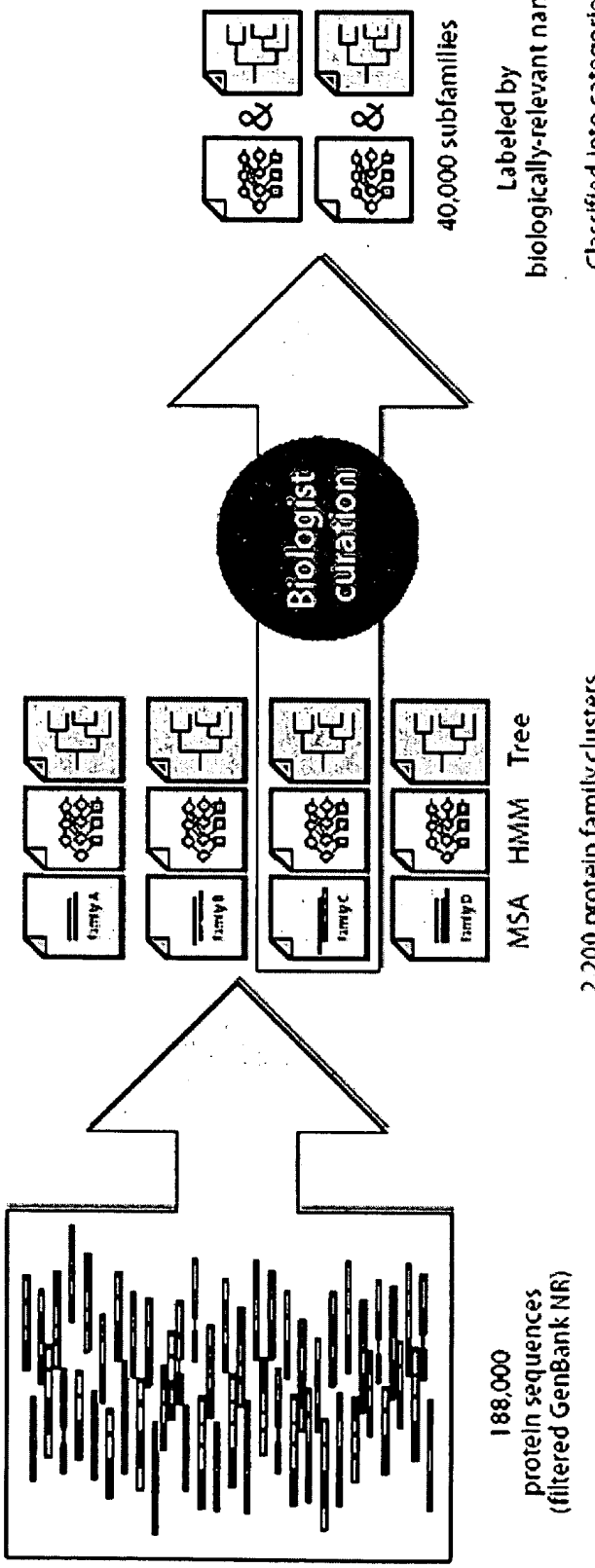


Figure - 48

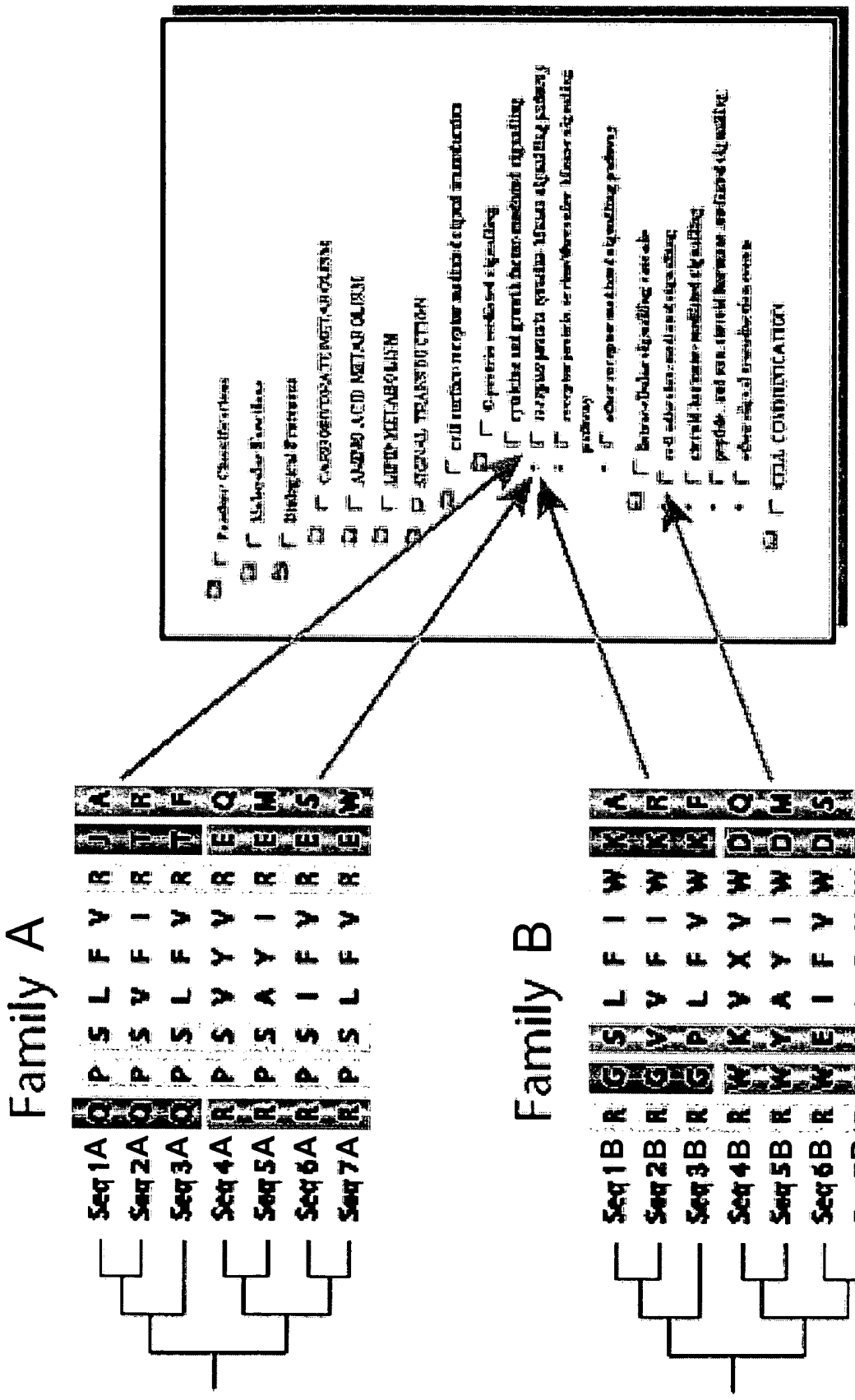


Figure - 49